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㉓ Vascular endothelial cells growth factor.

㉔ A novel protein of human origin produced by a human ovarian tumor established cell line HUOCA-II or HUOCA-III, which has a molecular weight, when determined by SDS-polyacrylamide gel electrophoresis, of from 72,000 to 80,000 daltons under a non-reducing condition or from 79,000 to 85,000 daltons under a reducing condition, which contains an amino acid sequence represented by the Sequence ID No. 4 deduced from the DNA sequence represented by the Sequence ID No. 5, and which enhances growth of vascular endothelial cells but does not activate growth of smooth muscle cells, fibroblasts and hepatocytes and also does not enhance or inhibit growth of HeLa cells. This invention also provides a process for the production of the protein.

FIELD OF THE INVENTION

This invention relates to a novel protein of human origin and its production process. Particularly, it relates to a novel proteinous angiogenic factor of human origin, which enhances the growth of vascular endothelial cells but does not activate the growth of other cells such as smooth muscle cells, fibroblasts, hepatocytes and the like, and to a process for the production thereof.

BACKGROUND OF THE INVENTION

Principal cells which constitute a blood vessel are vascular endothelial cells of tunica intima, smooth muscle cells of tunica media and fibroblasts of tunica externa. In addition, peripherally existing capillary blood vessels are composed solely of vascular endothelial cells. Though the mechanism of new formation of blood vessels, or angiogenesis, has not yet been elucidated in full details, it is considered that the angiogenesis starts firstly with dissolution of the blood vessel wall matrix and subsequent growth and migration of vascular endothelial cells.

Angiogenesis can be found during the prenatal period when new tissues and blood vessels are formed and at the time of the occurrence of physiological phenomena in the adult body such as periodical development of uterine endometrium and lutenization in ovaries, as well as under pathologic conditions such as chronic inflammation, wound healing and the like. New formation of blood vessels can also be found at the time of the growth of tumor cells. Endothelial cells which cover the inner wall of blood vessels are possessed of many physiological functions such as maintenance of anti-thrombotic activity, regulation of matter permeation, regulation of blood pressure and the like. In a patient suffering from a blood vessel-related disease such as arteriosclerosis, myocardial infarction or the like, abnormality can be found in these blood vessel-constituting cells.

A number of angiogenic factors have been found in the *in vivo* experimental systems for the formation of new blood vessels, such as an experiment in which chick chorio-allantoic membrane is used. For example, generally known proteinous angiogenic factors include basic fibroblast growth factor (bFGF), epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factor (TGF) and the like.

Though these prior art angiogenic factors having the ability to enhance formation of new blood vessels are possessed of the activity to enhance growth of vascular endothelial cells, these factors also strongly activate growth of other cells. For example, bFGF activates growth of various cells such as fibroblasts, smooth muscle cells, epidermal cells and the like. In consequence, each of these prior art angiogenic factors having a broad range of growth enhancing effects on various types of cells enhances not only the formation of new blood vessels but also the growth of other cells at the same time. In other words, these prior art factors have a problem of causing secondary reactions when used because of their inability to selectively enhance formation of new blood vessels.

Accordingly, the present invention contemplates overcoming the aforementioned problems involved in the prior art and, as the results, providing a purified angiogenic factor which enhances growth of vascular endothelial cells but does not or hardly activate growth of other cells such as smooth muscle cells, fibroblasts, hepatocytes and the like. The present invention also contemplates developing side effect-free pharmaceutical preparations and medical devices based on such a purified angiogenesis factor.

With the aim of accomplishing these objects, the inventors of the present invention have conducted intensive studies and found that products of human ovarian tumor established cell lines, HUOCA-II and HUOCA-III, were able to enhance growth of vascular endothelial cells selectively. The results have been disclosed in Japanese Patent Application Kokai Nos. 2-261375, 2262523 and 3-84000.

Thereafter, the present inventors have carried out studies on the purification of the aforementioned products of HUOCA-II and HUOCA-III cell lines from their serum-free culture supernatants, making use of specific purification techniques, and have succeeded in obtaining a highly purified specific protein having the aforementioned desirable properties, that is, having a strong activity to enhance growth of vascular endothelial cells but with no activity to activate growth of other cells such as smooth muscle cells, fibroblasts, hepatocytes and the like.

By further continuing the studies, a total RNA was isolated from the HUOCA-II or HUOCA-III cells and its cDNA was cloned. Thereafter, the DNA sequence of the cDNA was determined and its corresponding amino acid sequence was deduced, thereby succeeding in obtaining the novel protein of the present invention.

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SUMMARY OF THE INVENTION

According to a first aspect of the present invention, there is provided a single chain protein produced by

HUOCA-II or HUOCA-III, which has the following properties of:

- (1) having a molecular weight, when determined by SDS polyacrylamide gel electrophoresis, of from 72,000 to 80,000 daltons under a non-reducing condition or from 79,000 to 85,000 daltons under a reducing condition;
- (2) containing three peptide chains, respectively represented by the Sequence ID Nos. 1, 2 and 3 as attached hereto (in the Sequence ID No. 3, "Xaa" means an unidentified amino acid residue), in one molecule;
- (3) having an activity to enhance the growth of vascular endothelial cells;
- (4) having no activity to enhance the growth of fibroblasts; vascular smooth muscle cells and hepatocytes;
- (5) having no activity to enhance or inhibit the growth of HeLa cells; and
- (6) having an activity to enhance formation of new blood vessels.

According to a second aspect of the present invention, there is provided a protein of human origin which contains an amino acid sequence or a portion of the amino acid sequence represented by the Sequence ID No. 4 attached hereto that has been identified by isolating a corresponding total RNA molecule from HUOCA-II or HUOCA-III cells, cloning a cDNA corresponding to the proteins, determining the DNA sequence of the cDNA and deducing an amino acid sequence from the DNA sequence.

According to a third aspect of the present invention, there is provided a process for the production of a protein of human origin according to the first or second aspect of the present invention, which comprises purifying a serum-free culture supernatant of a human ovarian tumor cell or established cell line thereof, especially HUOCA-II or HUOCA-III, by an optional combination of purification techniques including (a) cation exchange chromatography, (b) heparin affinity chromatography, (c) heparin affinity high performance liquid chromatography and (d) reverse phase high performance liquid chromatography, or which comprises the steps of (i) preparing a DNA fragment containing a nucleotide sequence which encodes the protein or a portion of the protein shown in the Sequence ID No. 4 attached hereto, (ii) obtaining a transformant by transforming cells of a host with the DNA fragment prepared in the above step (i) or with a vector containing the DNA fragment and (iii) culturing the transformant obtained in the above step (ii) to allow the transformant to produce the protein of the Sequence ID No. 4, or a portion of the protein, subsequently recovering the protein from resulting culture mixture.

According to a fourth aspect of the present invention, there is provided a pharmaceutical preparation which contains the protein or a portion of the protein of the first and/or second aspect of the present invention as an active ingredient.

According to a fifth aspect of the present invention, there is provided a DNA fragment or cDNA-fragment which contains a nucleotide sequence or a portion of the nucleotide sequence represented by the Sequence ID No. 5 attached hereto wherein at least one base may be substituted based on the degeneracy of genetic code.

According to a sixth aspect of the present invention, there is provided an expression vector containing the DNA fragment, as well as a transformant transformed with the DNA fragment or the expression vector.

Other objects and advantages of the present invention will be made apparent as the description progresses.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a graph showing the absorbance, measured at a wave length of 280 nm, of each eluate fraction resulting from the treatment of an HUOCA-III serum-free culture supernatant with cation exchange chromatography.

Fig. 2 is a graph showing the results of the measurement of activities in the eluate fractions obtained in Fig. 1 to enhance the growth of vascular endothelial cells.

Fig. 3 is a graph showing the absorbance, measured at a wave length of 280 nm, of each eluate fraction resulting from a heparin affinity chromatographic treatment of the active fractions of the cation exchange chromatography eluates having the vascular endothelial cell growth-enhancing activity.

Fig. 4 is a graph showing the results of the measurement of activities in the eluate fractions obtained in Fig. 3 to enhance the growth of vascular endothelial cells.

Fig. 5 is a graph showing the absorbance, measured at a wave length of 215 nm, of each eluate fraction resulting from a heparin affinity high performance liquid chromatographic treatment of the active fractions of the heparin affinity chromatography eluates having the vascular endothelial cell growth-enhancing activity.

Fig. 6 is a graph showing the results of the measurement of activities in the eluate fractions obtained in Fig. 5 to enhance growth of vascular endothelial cells.

Fig. 7 is a graph showing the absorbance, measured at a wave length of 215 nm, of each eluate fraction

resulting from a reverse phase high performance liquid chromatographic treatment of the active fractions of the heparin affinity high performance liquid chromatography eluates having the vascular endothelial cell growth-enhancing activity.

Fig. 8 is a graph showing the results of the measurement of activities in the eluate fractions obtained in Fig. 7 to enhance the growth of vascular endothelial cells.

Fig. 9 is a graph showing an SDS polyacrylamide gel electrophoresis pattern of a highly purified product (glycoprotein) obtained in Example 1 of the present invention.

Fig. 10 is a graph showing results of the measurement of the vascular endothelial cell growth-enhancing activity of the highly purified product eluted from each cut portion of the electrophoresis gel of Fig. 9.

Fig. 11 is a graph showing an SDS-polyacrylamide gel electrophoresis pattern of an N-glycanase-treated product of the highly purified product (glycoprotein) obtained in Example 1 of the present invention.

Fig. 12 represents the nucleotide sequence of the mRNA from which the cDNA obtained in Example 1 step (B) is translated and the corresponding amino acid sequence deduced from the nucleotide sequence.

15 DETAILED DESCRIPTION OF THE INVENTION

Firstly, a first and a second aspects of the present invention are described in detail.

The gist of the first aspect of the present invention resides in a single chain protein produced by HUOCA-II or HUOCA-III, which has the following properties of:

- (1) having a molecular weight, when determined by SDS polyacrylamide gel electrophoresis, of from 72,000 to 80,000 daltons under a non-reducing condition or from 79,000 to 85,000 daltons under a reducing condition;
- (2) containing three peptide chains, respectively represented by the Sequence ID Nos. 1, 2 and 3 as attached hereto (in the Sequence ID No. 3, "Xaa" means an unidentified amino acid residue), in one molecule;
- (3) having an activity to enhance the growth of vascular endothelial cells;
- (4) having no activity to enhance the growth of fibroblasts, vascular smooth muscle cells and hepatocytes;
- (5) having no activity to enhance or inhibit the growth of HeLa cells; and
- (6) having an activity to enhance the formation of new blood vessels.

The gist of the second aspect of the present invention resides in a protein of human origin which contains an amino acid sequence or a portion of the sequence represented by the Sequence ID No. 4 attached hereto that has been identified by isolating a corresponding mRNA molecule from HUOCA-II or HUOCA-III cells, cloning a gene corresponding to the mRNA, determining the DNA sequence of the gene and deducing an amino acid sequence from the DNA sequence.

The human ovarian tumor established cell lines HUOCA-II and HUOCA-III have been deposited by the present inventors on March 1, 1989, in Fermentation Research Institute, Agency of Industrial Science and Technology, and have been assigned the designations as FERM BP-2310 and FERM BP-2311. Though culturing of the HUOCA-II and HUOCA-III and preparation of their serum-free culture supernatants may be carried out in the usual way, these techniques are disclosed in detail by the present inventors in Japanese Patent Application Kokai Nos. 2-261375, 2-262523 and 3-84000.

The protein of the present invention comprises a single chain protein molecule, and the single chain protein contains three peptide chains respectively represented by the Sequence ID Nos. 1, 2 and 3 as attached hereto.

The protein of the present invention may be prepared from a serum-free culture supernatant of the human ovarian tumor established cell line, HUOCA-II or HUOCA-III, by subjecting the supernatant to a series of purification steps including (a) cation exchange chromatography, (b) heparin affinity chromatography, (c) heparin affinity high-performance liquid chromatography and (d) reverse-phase high-performance liquid chromatography. Preferably, it may be prepared in accordance with the following illustrative steps (i) to (iv).

Preparation of protein

- (i) A serum-free culture supernatant of HUOCA-II or HUOCA-III is adsorbed on to a cation exchange resin packed in a column. In this instance, the cation exchange resin may be either strongly ionic or weakly ionic, but the use of S-Sepharose® (trademark of Pharmacia) is particularly preferred. The thus adsorbed portion onto a cation exchange resin in the column is washed with an appropriate buffer solution and then subjected to a linear gradient elution using two buffer solutions respectively containing 150 mM NaCl and 2 M NaCl to collect active fractions showing the activity to enhance the growth of vascular endothelial cells [step (a)].
- (ii) The active fractions obtained in the above step (i) are pooled and diluted by a factor of 2 to 3 with the

same buffer solution containing 150 mM of NaCl. The thus diluted sample is applied to a heparin-Sepharose column, washed with the same buffer solution containing 0.5 M NaCl and then subjected to a linear gradient elution using two buffer solutions respectively containing 0.5 M NaCl and 2 M NaCl to collect active fractions showing the activity to enhance the growth of vascular endothelial cells [step (b)].

5 (iii) The active fractions obtained in the above step (ii) are diluted in the same manner, applied to a heparin column for high performance liquid chromatography use and then subjected to elution in the same manner to collect active fractions showing the activity to enhance the growth of vascular endothelial cells [step (c)].

10 (iv) The active fractions obtained in the above step (iii) are applied to a column for reverse-phase high-performance liquid chromatography use to obtain a purified product (protein) having the activity to enhance the growth of vascular endothelial cells [step (d)].

Any usually used buffer solution such as a phosphate buffer or the like may be used in the above glycoprotein preparation steps, and Sepharose or any other general purpose carrier may be used as a carrier of heparin.

15 The thus purified product has been identified as a glycoprotein, namely a sugar chain-attached protein molecule, on the basis of the facts that (1), when the purified product was allowed to react with a sugar chain-hydrolyzing enzyme N-glycanase and the resulting product was analyzed by 0.1% SDS-containing 10% polyacrylamide gel electrophoresis, the electrophoresis pattern of the thus treated product showed a decreased molecular weight level due to the digestion of sugar chains and (2) the purified product showed an affinity for concanavalin A.

In addition, the protein portion of the glycoprotein of the present invention was identified as a single chain protein molecule, because the purified product showed a single band when analyzed by 0.1% SDS-containing 10% polyacrylamide gel electrophoresis under reducing conditions.

20 Though the amino acid sequence of the protein portion of the thus obtained glycoprotein could be determined by any usually used means, the following illustrative steps (1) to (3) were employed herein in that order.

Determination of amino acid sequence

(1) Reductive carboxymethylation

30 The sample purified and isolated in the aforementioned step (iv) by reverse-phase high-performance liquid chromatography was concentrated using a concentrator and eluted with an eluting solution consisting of 8 M urea, 0.5 M Tris-HCl pH 8.0 and 1 mM EDTA. To this was added dithiothreitol to a final concentration of 20 mM. After nitrogen gas flush, the reduction reaction was carried out in the dark for 2 hours at room temperature.

35 Thereafter, monoiidoacetic acid was added to the resulting reaction mixture to a final concentration of 20 mM, and the alkylation reaction was carried out in the dark for 30 minutes at room temperature.

(2) Digestion with lysyl endopeptidase

40 The reductive alkylation product obtained in the above step (1) was mixed with 2-mercaptoethanol, followed by the addition of 0.1 N NaOH to adjust the mixture to pH 8.5. Lysyl endopeptidase (Wako Pure Chemical Industries, Ltd.) was added in a 1:10 (w/w) ratio to the thus prepared substrate to carry out the enzymatic hydrolysis reaction at 37°C for 4 hours.

45 (3) Fractionation of peptide fragments and determination of the amino acid sequence

The peptide fragments mixture obtained in the above step (2) were separated by reverse-phase high-performance chromatography using an RP300 column (Applied Biosystems, Inc.). The elution was carried out by linear concentration gradient of acetonitrile from 0% to 60% in the presence of 0.1% TFA. The thus obtained peptide fragments by the elution treatment were subjected to Edman degradation using a gas phase sequencer (Model 477A; Applied Biosystems, Inc.), and the resulting PTH-amino acids were identified using a high-performance liquid chromatography for PTH-amino acid identification use (Model 120A; Applied Biosystems, Inc.). As the results, it was found that the protein portion of the glycoprotein of the present invention contained three peptide chains respectively represented by the Sequence ID Nos. 1, 2 and 3.

Determination of the complete DNA sequence by PCR

The amino acid sequence determined in the above step (3) coincided well with that of human hepatocyte

growth factor (hHGF). With regard to hHGF, its cDNA sequence has been reported by Nakamura (*Nature*, vol.342, pp.440 - 443, 1989) and Miyazawa (*Biochemical and Biophysical Research Communication*, vol.163, pp.967 - 973, 1989).

5 Since several cDNA nucleotide sequences have been reported on the hHGF family, primers for PCR use were prepared using a DNA synthesizer based on the common sequences in the 5' and 3' non-translation regions of these known nucleotide sequences. That is, primers were synthesized based on a region including 47 to 82 position bases (5' primer) counting in upstream direction from the 5' end of the translation region (translation initiation point) and another region including 1 to 37 position bases (3' primer) counting in downstream direction from the 3' end.

10 The total RNA sample was prepared from the human ovarian tumor cell line HUOCA-III by means of an SDS-phenol method. Using the thus prepared total RNA as a template, cDNA synthesis was carried out making use of M-MLV reverse transcriptase. The thus synthesized cDNA was subjected to PCR and the resulting PCR product was applied to agarose gel electrophoresis to find a DNA fragment having a size of about 2.3 kb. Since the open reading frame of the HGF family so far reported has a size of about 2.3 kb, this DNA fragment was 15 considered to be a cDNA molecule coding for the HUOCA-III-originated novel protein of the present invention. In consequence, this DNA fragment was purified from the agarose gel, inserted into the pJC18 plasmid vector and then transformed into *Escherichia coli* JM109. Some of the thus obtained clones were examined making use of the dideoxy method to determine their nucleotide sequences. By correcting reading errors at the time of the PCR study, a nucleotide sequence corresponding to the novel protein of HUOCA-III origin was determined. The thus determined nucleotide sequence is shown in the Sequence ID No. 5 attached hereto, and an amino acid sequence deduced from the nucleotide sequence in the Sequence ID No. 4.

Measurement of molecular weight by SDS-polyacrylamide gel electrophoresis

25 Electrophoresis was carried out using a 10% polyacrylamide gel in accordance with the procedure of Lam-meli et al. (*Nature*, vol.277, pp.680 - 685, 1970). The resulting gel was fixed by treating it with 50% ethanol and 40% acetic acid for 30 minutes, washed with 10% ethanol and 5% acetic acid and then subjected to silver staining. The protein of the present invention was stained as a single band, and its molecular weight was estimated to be about 72,000 to 80,000 daltons based on its relative mobility. In addition, another electrophoresis 30 was carried out under a reducing condition by adding 2-mercaptoethanol to the sample to a concentration of 5% and treating the mixture at 95°C for 10 minutes, followed by the same procedure as the case of the above non-reducing condition. Under the reducing condition, the molecular weight of the protein of the present invention was estimated to be about 79,000 to 85,000 daltons.

35 Next, a third aspect of the present invention is described in the following.

35 The gist of the third aspect of the present invention resides in a process for the production of the protein of the first or second aspect of the present invention.

Firstly, a culture mixture containing the protein of the first or second aspect of the present invention is obtained.

40 The single chain protein of the first aspect of the present invention is obtained by recovering it from a serum-free culture supernatant of the human ovarian tumor cell line, HUOCA-II or HUOCA-III.

The novel protein of the second aspect of the present invention is obtained by preparing a DNA fragment containing a nucleotide sequence which encodes the novel protein represented by the amino acid sequence or a portion of the sequence shown in the Sequence ID No. 4, preferably the DNA fragment or a portion of the DNA fragment represented by the Sequence ID No. 5, transforming appropriate host cells with the thus ligated 45 fragment directly or indirectly using a proper expression vector, culturing the thus obtained transformant and then recovering the novel protein of the Sequence ID No. 4 from the resulting culture mixture.

The recovering step may be effected, though not particularly limited, by purifying the novel protein by means of (a) cation exchange chromatography, (b) heparin affinity chromatography, (c) heparin affinity high-performance liquid chromatography and (d) reverse-phase high-performance liquid chromatography, in any optional combination in order.

50 According to a fourth aspect of the present invention, there is provided a pharmaceutical preparation which contains the protein of the first and/or second aspect of the present invention as an active ingredient.

The pharmaceutical preparation may be applied to various dosage forms such as tablets, sugar coated tablets, powders, capsules, granules, suspensions, emulsions, parenteral solutions, external preparations, ointments and the like, using the preparation alone or together with other necessary ingredients in combination with appropriate carriers, fillers and the like.

55 The protein of the present invention is possessed of a function to enhance vascular endothelial cell growth in human and various animals, but does not enhance the growth of fibroblasts, vascular smooth muscle cells

or hepatocytes in human and animals and does not enhance or inhibit the growth of HeLa cells. Because of such nature, the growth of vascular endothelial cells can be enhanced selectively and, as the results, new formation of blood vessels can be effected smoothly without causing secondary reactions.

The term "it does not enhance the growth of fibroblasts; vascular smooth muscle cells or hepatocytes and does not enhance or inhibit the growth of HeLa cells" as used herein includes two cases; one case meaning that it does not enhance the growth of fibroblasts, vascular smooth muscle cells or hepatocytes and does not enhance or inhibit the growth of HeLa cell at all, and the other case meaning that it shows these activities to some extent but to an extremely small degree in comparison with its activity to enhance the growth of vascular endothelial cells.

10 Illustrative procedures for the measurement of activities of the protein of the present invention to enhance the growth of vascular endothelial cells, fibroblasts, vascular smooth muscle cells, hepatocytes and HeLa cells and to inhibit the growth of HeLa cells will be described later in detail in Examples.

In addition to the above properties, the protein of the present invention shows an affinity for concanavalin A. In the present invention, the affinity for concanavalin A was examined in the following manner.

15 Measurement of affinity for concanavalin A

Using a dot blot apparatus (BioDot; Bio-Rad Laboratories, Inc.), a 500 ng portion of the purified product described in the foregoing was adsorbed to a nitrocellulose membrane (Bio-Rad Laboratories, Inc.) which has in advance been soaked in 10 mM Tris-HCl buffer (pH 7.5) containing 0.15 M NaCl. After air-drying, the resulting membrane was washed by soaking it for 10 minutes in 10 mM Tris-HCl buffer (pH 7.5) containing 0.15 M NaCl and 0.05% Tween and then replacing the washing buffer by a fresh one. After repeating the washing step 4 times, the membrane was soaked for 1 hour at 4°C in the same buffer which has been further supplemented with 1% BSA (bovine serum albumin), and washed again.

20 The thus treated membrane was soaked in a solution containing 10 µg/ml of labelled horseradish peroxidase (HRP) - concanavalin A at 4°C for 1 hour and washed again. Thereafter, the HRP remaining after the washing was allowed to perform a coloring reaction in the presence of H₂O₂ using 3,3'-diaminobenzidine as a substrate, in order to judge the affinity of the inventive protein for concanavalin A. As the results, the purified product blotted on the membrane showed development of a brown color, while a control test resulted in no coloration, thus confirming the affinity of the purified product for concanavalin A.

25 As described in the foregoing, the protein of the present invention is possessed of excellent ability to enhance vascular endothelial cells growth as well as its function to enhance new formation of blood vessels. Because of such nature, a physiologically active pharmaceutical preparation containing the inventive protein can be used as a healing enhancer of wound, burn injury, decubitus, postoperative tissue damage or the like or as a drug for the treatment of cardiac angiopathy, as well as its application to artificial organs such as artificial blood vessel, artificial skin and the like. In addition, antibodies specific for the protein of the present invention and inhibitors of the inventive protein can be used effectively as diagnostic and therapeutic drugs of malignant tumor, retinopathy, chronic rheumatoid arthritis and the like.

40 EXAMPLES

The following examples are provided to further illustrate the preparation process of the protein of the present invention, the measurement of its molecular weight, its activities on various cells and the presence or absence of its sugar chain moiety. It is to be understood, however, that the examples are for purpose of illustration only and are not intended as a definition of the limits of the invention.

Example 1

50 (A) Preparation of the protein, measurement of its molecular weight and determination of its aminoacid sequence

(1) To 10 liters of HUOCA-III serum-free culture supernatant was added CHAPS (3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulfonate; Dojin Kagaku K.K.) to a final concentration of 0.03%. The thus prepared serum-free culture supernatant was applied to a 40 ml volume of S-Sepharose (Fast Flow, Pharmacia) which has been equilibrated in advance with 10 mM phosphate buffer (pH 7.2) containing 0.15 M NaCl and 0.03% CHAPS, and the contents were adsorbed at a flow rate of 200 ml/hour at 4°C. After washing with the just described buffer solution containing 0.15 M NaCl, the adsorbed contents were eluted by a linear NaCl gradient using two buffers containing 0.15 M NaCl and 2.0 M NaCl at a flow rate of 200 ml/hour

and at a temperature of 4°C. The eluate was checked for its absorbance at 280 nm and collected as fractions of 6.7 ml/tube. Results of the absorbance measurement at 280 nm are shown in Fig. 1.

Each of the thus collected fractions was checked for its activity to enhance the growth of bovine aorta endothelial cells in the following manner. As shown in Fig. 2, the cell growth enhancing activity was found mostly in fractions 12 to 24.

Measurement of activity to enhance the growth of bovine aorta endothelial cells

Bovine aorta endothelial cells were suspended in DME (Dulbecco's Modified Eagle's) medium (Flow Laboratories, Inc.) which has been supplemented with 10% fetal calf serum, and the cell suspension was poured in a 24 well multi-dish (Corning Glassworks) with a density of 5×10^3 cells/well. On the following day, the medium was replaced by fresh DME medium containing 5% fetal calf serum, and a sample to be tested was added to the fresh medium, followed by 4 days of culturing to measure the number of resulting cells.

(2) The fractions obtained in the above step (1) having high vascular endothelial cell growth-enhancing activities were pooled and diluted with a buffer solution by a factor of 3, and the contents were adsorbed to heparin-Sepharose CL-6B (Pharmacia; bed volume, 4 ml) which has been equilibrated in advance with a buffer solution containing 0.5 M NaCl, at a flow rate of from 0.2 to 0.4 ml/minute and at a temperature of 4°C. After washing with the same buffer solution containing 0.5 M NaCl, the adsorbed contents were eluted by a linear NaCl gradient using two buffers containing 0.5 M NaCl and 2.0 M NaCl at a flow rate of 0.2 ml/min and at a temperature of 4°C. The eluate was checked for its absorbance at 280 nm and collected as fractions of 3 ml/tube. Results of the absorbance measurement at 280 nm are shown in Fig. 3.

Each of the thus collected fractions was checked for its activity to enhance the growth of bovine aorta endothelial cells in the same manner as described above. As shown in Fig. 4, the cell growth enhancing activity was found mostly in fractions 23 to 30.

(3) The fractions obtained in the above step (2) having high vascular endothelial cell growth-enhancing activities were pooled and diluted with a buffer solution by a factor of 3, and the contents were adsorbed on to a TSK-heparin 5PW column (7.5 mm in inside diameter and 7.5 cm in length; Tosoh Corp.) which has been equilibrated in advance with a buffer solution containing 0.5 M NaCl. After washing with the same buffer solution containing 0.5 M NaCl, the adsorbed contents were eluted by a linear NaCl gradient using two buffers containing 0.5 M NaCl and 2.0 M NaCl, at a flow rate of 0.5 ml/min and at room temperature. The eluate was checked for its absorbance at 215 nm and collected as fractions of 0.5 ml/tube. Results of the absorbance measurement at 215 nm are shown in Fig. 5.

Each of the thus collected fractions was checked for its activity to enhance the growth of bovine aorta endothelial cells in the same manner as described above. As shown in Fig. 6, the cell growth enhancing activity was found mostly in fractions 30 to 32.

(4) The fractions obtained in the above step (3) having high vascular endothelial cell growth-enhancing activities were pooled and subjected to reverse phase chromatography using a vp-318 column (4.6 mm in inside diameter and 30 mm in length; Senshu Kagaku Co., Ltd.). In the presence of 0.1% trifluoroacetic acid (TFA), a linear gradient elution was carried out by increasing the concentration of acetonitrile from 10% to 60%, at a flow rate of 1.0 ml/min. The eluate was checked for its absorbance at 215 nm and collected as fractions of 10 ml/tube. Results of the absorbance measurement at 215 nm are shown in Fig. 7.

Each of the thus collected fractions was checked for its activity to enhance the growth of bovine aorta endothelial cells in the same manner as described above, with the results shown in Fig. 8. By collecting peak fractions, a highly purified product having high vascular endothelial cell growth-enhancing activity was obtained.

(5) The molecular weight of the highly purified product obtained in the above step (4) was measured by SDS polyacrylamide gel electrophoresis.

The following 6 authentic samples whose molecular weights have been confirmed were used as molecular weight markers, and the electrophoresis was carried out in the same manner as described in the foregoing.

[Molecular weight markers]	
5	1. Rabbit muscle phosphorylase (M.W., 97,400 daltons)
	2. Bovine serum albumin (M.W., 66,200 daltons)
	3. Ovalbumin (M.W., 45,000 daltons)
10	4. Carbonic anhydrase (M.W., 31,000 daltons)
	5. Soybean trypsin inhibitor (M.W., 21,500 daltons)
	6. Lysozyme (M.W., 14,400 daltons)

The thus obtained electrophoresis pattern is shown in Fig. 9. As is evident from the figure, the highly purified product obtained in the above step (4) has a molecular weight of 72,000 to 80,000 daltons under non-reducing condition, or 79,000 to 85,000 daltons under reducing condition, when measured by SDS polyacrylamide gel electrophoresis. It is evident also that the purified product is a single chain protein.

After the electrophoresis, the gel was cut out at intervals of 2 mm. Each of the thus cut portions was put into a test tube, ground into pieces, mixed with 500 μ l of a buffer solution 0.03% CHAPS, 20 mmol PB pH 7.2 and then shaken at 4°C for 16 hours. The resulting mixture was centrifuged to recover supernatant fluid which was subsequently dialyzed against a buffer solution 0.03% CHAPS, 20 mmol PB pH 7.2. Contents in the thus dialyzed solution was freeze-dried and then dissolved in 100 μ l of a buffer solution 0.03% CHAPS, 20 mmol PB pH 7.2 to measure the activity to enhance the growth of bovine aorta endothelial cells in the same manner as described in the foregoing. As shown in Figure 10, the endothelial cell growth-enhancing activity was observed in 72,000-80,000 molecular weight fraction obtained under non-reducing condition.

When the amino acid sequence of the highly purified product was determined in accordance with the procedure described in the foregoing, it was confirmed that the product contained three peptide chains respectively represented by the Sequence ID Nos. 1, 2 and 3.

Also, in order to confirm the addition of sugar chains to the highly purified product, 5 μ l (250 ng) of the high purity product and 3.2 μ l of N-glycanase (Genzyme Corp.; 250 units/ml) were added to 30 μ l of 50 mM Tris-HCl buffer (pH 8.0). After 18 hours of reaction, the resulting mixture was subjected to 0.1% SDS-10% polyacrylamide gel electrophoresis, followed by silver staining. As shown in Fig. 11, the resulting electrophoresis pattern clearly indicated a decrease in the molecular weight of the N-glycanase-treated product due to the separation of sugar chains.

35 (B) Cloning of the DNA and estimation of the amino acid sequence

(a) Synthesis of the cDNA

40 A 5 μ l portion of the total RNA sample (10 μ g/ μ l) which has been prepared from the human ovarian tumor cell line HUOCA-III by the SDS-phenol method was incubated at 70°C for 5 minutes and then cooled down rapidly. After 5 minutes of cooling on an ice bath, to this were added 10 μ l of a 5 x buffer solution for reverse transcription use (250 mM Tris-HCl/pH 8.3, 375 mM KCl, 15 mM MgCl₂), 15 μ l of 2.5 mM dNTP (a mixture of dATP, dCTP, dGTP and dTTP; Takara Shuzo Co., Ltd.), 0.5 μ l of 1 M DTT (dithiothreitol), 1 μ l of oligo(dT)₁₂₋₁₈ (Amersham), 2.5 μ l of a ribonuclease inhibitor (200 U/ μ l, Takara Shuzo Co., Ltd.), 13 μ l of distilled water and 3 μ l of M-MLV reverse transcriptase (200 U/ μ l, GIBCO-BRL). The thus prepared mixture was incubated at 37°C for 1 hour to effect cDNA synthesis. After removing the proteinous materials from the resulting reaction mixture by phenol treatment, the cDNA of interest was recovered by ethanol precipitation, dissolved in 50 μ l of distilled water and then stored at -80°C.

50 (b) Amplification of the cDNA which encodes the HUOCA-III-originated novel protein by polymerase chain reaction (PCR)

To 5 μ l of the cDNA aqueous solution were added 70 μ l of distilled water, 10 μ l of a 10 x buffer solution for PCR use (500 mM KCl, 15 mM MgCl₂, 100 mM Tris-HCl/pH 8.3, 0.01% (w/v) gelatin), 8 μ l of dNTP (Takara Shuzo Co., Ltd.), 3 μ l of a 5' primer (5' TCTTTAGGCACTGACTCCGAACAGGATTCTTCAC 3', 1 μ g/ μ l) and 3 μ l of a 3' primer (5' GTTGTATTGGTGGATCCTTCAAGACACACTTACTTCAG 3'). The thus prepared mixture was incubated at 95°C for 7 minutes, followed by rapid cooling. The thus treated solution was mixed with 1 μ l

of Ampli Taq DNA polymerase (5 U/ μ l, Perkin Elmer Cetus), and the surface of the reaction solution was covered with mineral oil (nujol mineral oil manufactured by Perkin Elmer Cetus). Thereafter, PCR was carried out by 30 repetitions of a three step reaction (94°C for 1 minute, 60°C for 2 minutes and 72°C for 3 minutes). After completion of the reaction, mineral oil was removed by chloroform treatment, proteinous materials were removed by phenol treatment and then the PCR product was recovered by ethanol precipitation.

5 (c) Digestion of the PCR product with BamHI

An 85 μ l portion of the PCR product was mixed with 10 μ l of a 10 x buffer solution for BamHI reaction use (1.5 M NaCl, 60 mM Tris-HCl/pH 7.9, 60 mM MgCl₂) and 5 μ l of an aqueous solution of BamHI (15 U/ μ l, Nippon Gene), and the resulting mixture was incubated at 37°C for 1 hour.

10 (d) Purification of the BamHI-digested PCR product

15 The PCR product thus digested with BamHI was subjected to 0.7% agarose gel electrophoresis at a constant voltage (100 V). After completion of the electrophoresis, the gel was stained with ethidium bromide to observe DNA bands using a UV transilluminator. A portion of the gel where a DNA band of 2.3 kb was observed was cut out, and the PCR product in the cut portion was purified using Sephaglas Band Prep Kit (Pharmacia).

20 (e) Digestion of the pUC18 plasmid vector with BamHI

A 2 μ l portion of pUC18 solution (1 μ g/ μ l, Takara Shuzo Co., Ltd.) was mixed with 6.6 μ l of distilled water, 3 μ l of the 10 x buffer solution for BamHI reaction use and 1.4 μ l of BamHI (15 U/ μ l, Nippon Gene), and the resulting mixture was incubated at 37°C for 1 hour to digest the plasmid. After completion of the reaction, proteinous materials were removed by phenol treatment and the thus digested plasmid fragments were recovered by ethanol precipitation. The thus recovered plasmid fragments were dissolved in 33 μ l of distilled water and mixed with 4 μ l of CIP buffer (50 mM Tris-HCl/pH 8.0, 1 mM MgCl₂) and 3 μ l of alkaline phosphatase (calf intestine origin, 2,500 U/ml, Toyobo Co., Ltd.). The resulting mixture was incubated at 37°C for 40 minutes and then at 50°C for 20 minutes. After completion of the reaction, the BamHI-digested fragments of the plasmid vector pUC18 were recovered by phenol treatment and subsequent ethanol treatment.

30 (f) Transformation of E.Coli JM109 with the PCR product

To 6 μ l (30 μ g) of the the BamHI-digested PCR product were added 2 μ l (200 μ g) of the pUC18 digest prepared in the above step (e), 2 μ l of a 10 x ligation buffer solution (10 mM ATP, 200 mM DTT, 100 mM MgCl₂, 500 mM Tris-HCl/pH 7.9), 9 μ l of distilled water and 1 μ l of T4 DNA ligase (500 U/ μ l, Nippon Gene). After overnight reaction at 16°C, a portion of the resulting reaction solution was added to 100 μ l of a suspension of E.coli JM109 competent cells (Nippon Gene). The thus prepared mixture was allowed to stand still for 20 minutes on an ice bath, heat-treated at 42°C for 45 seconds and then allowed again to stand still on an ice bath for at least 2 minutes. The thus treated mixture was added to 400 μ l of High-competence broth (Nippon Gene) and stirred on a shaker at 37°C for 60 minutes. To this were added 40 μ l of 2% X-Gal (5-bromo-4-chloro-3-indolyl- β -D-galactopyranoside) dissolved in diethylformamide and 40 μ l of 100 mM IPTG (isopropyl- β -D-thio-galactopyranoside). The thus prepared mixture was poured on LB plate medium (0.5% yeast extract, 1% Bacto-Tryptone, 1.5% agar, 1% NaCl, 50 μ g/ml ampicillin, pH 7.5) and incubated overnight at 37°C to find white (recombinant) colonies and blue (non-recombinant) colonies grown on the medium. By isolating white colonies, a JM109 transformant into which the cDNA of interest has been inserted was selected.

40 (g) Preparation of the plasmid

50 The plasmid-introduced JM109 was cultured overnight at 37°C in 100 ml of LB medium (1% Bacto-Tryptone, 0.5% yeast extract, 1% NaCl, pH 7.5). When the cells reached their logarithmic growth phase, they were collected by centrifugation (5 minutes, 5,000 rpm, 0°C) and suspended in 4 ml of P1 buffer solution (100 μ g/ml RNase A, 50 mM Tris-HCl/pH 8.0, 10 mM EDTA). The resulting cell suspension was mixed with 4 ml of P2 buffer solution (200 mM NaOH, 1% SDS) to carry out an alkali treatment at room temperature for 5 minutes. After the alkali denaturation, the resulting mixture was neutralized by adding 4 ml of P3 buffer solution (2.55 mM Potassium acetate, pH 4.8) and then centrifuged at 15,000 rpm for 30 minutes at 4°C. The thus obtained supernatant fluid was applied to a QIAGEN-MIDI column-pack 100 (QIAGEN) which has been equilibrated in advance with 2 ml of QB buff r solution (750 mM NaCl, 50 mM MOPS [3-(N-morpholino)propanesulfonic acid]/pH

7.0, 15% ethanol). After washing the column twice with 4 ml of QC buffer solution (1 M NaCl, 50 mM MOPS/pH 7.0, 15% ethanol), the plasmid was eluted with 2 ml of QF buffer solution (1.2 M NaCl, 15% ethanol, 50 mM MOPS/pH 8.0). The eluate was mixed with 500 μ l of isopropanol and centrifuged at room temperature for 30 minutes. Thereafter, the precipitate thus obtained was washed with 70% ethanol and dissolved in 100 μ l of distilled water.

5 (h) Determination of the nucleotide sequence by the dideoxy method

A 16 μ l (3 μ g) portion of the plasmid solution prepared in the above step (g) was mixed with 2 μ l of 2 N 10 NaOH and 2 μ l of 2 mM EDTA, and the mixture was incubated at 37°C for 25 minutes to denature the plasmid. After the alkali denaturation, the resulting solution was mixed with 2 μ l of 3 M sodium acetate and 100 μ l of cold ethanol, and ethanol precipitation was effected by maintaining the mixture for 10 minutes at -80°C. The thus precipitated plasmid was recovered by centrifugation, washed with 70% ethanol and then dissolved in 7 μ l of distilled water. To this were added 1 μ l of a primer (0.5 pmole) and 2 μ l of a 5 x buffer solution A (250 mM 15 NaCl, 200 mM Tris-HCl/pH 7.5, 100 mM MgCl₂). After 2 minutes of incubation at 65°C, the resulting solution was gradually cooled down to 30°C to effect annealing of the denatured plasmid and the primer. To the resulting solution were added 1 μ l of 0.1 M dithiothreitol, 2 μ l of a labeling mixture (1.5 μ M 7-deaza-dGTP, 1.5 μ M dATP, 1.5 μ M dTTP, 0.5 μ M of [α -³²P]dCTP (1,000 Ci/mmol, Amersham) and 2 μ l of Sequenase Ver. 2.0 (1.5 μ U/ml, United States Biochemical Corporation). After 5 minutes of reaction at 37°C, a 3.5 μ l portion of the resulting 20 reaction mixture was added to 2.5 μ l of each of a G solution (80 μ M 7-deaza-dGTP, 80 μ M dATP, 80 μ M dCTP, 80 μ M dTTP, 8 μ M ddGTP, 50 mM NaCl), an A solution (80 μ M 7-deaza-dGTP, 80 μ M dATP, 80 μ M dCTP, 80 μ M dTTP, 8 μ M ddATP, 50 mM NaCl), a C solution (80 μ M 7-deaza-dGTP, 80 μ M dATP, 80 μ M dCTP, 80 μ M dTTP, 8 μ M ddCTP, 50 mM NaCl) and a T solution (80 μ M 7-deaza-dGTP, 80 μ M dATP, 80 μ M dCTP, 80 μ M dTTP, 8 μ M ddTTP, 50 mM NaCl). In this instance, each of these solutions was kept at 37°C prior to its use. 25 After 5 minutes of reaction at 37°C, the reaction was terminated by adding 4 μ l of a reaction termination solution (95% formamide, 0.05% Bromophenol Blue, 20 mM EDTA, 0.05% Xylene Cyanol FF). Thereafter, the reaction mixture was heated at 90°C for 5 minutes, followed by rapid cooling, and a 2.5 μ l portion of the resulting sample was subjected to electrophoresis. In this case, a composition consisting of 7 M urea, 10% HydroLink™ LONG-RANGER (AT Biochem), 100 mM Tris-HCl, 100 mM boric acid and 2 mM EDTA was made into gel according to 30 0.05% ammonium persulfate and 0.0005% N,N,N',N'-tetramethylenediamine (TEMED), and the electrophoresis was carried out at a constant power of 60 W using a TEB buffer (50 mM Tris, 50 mM boric acid, 1 mM EDTA). After completion of the electrophoresis, the gel was dried on a filter paper and subjected to autoradiography to determine the nucleotide sequence of the DNA of interest.

The thus determined DNA sequence is shown in the Sequence ID No. 5, and an amino acid sequence 35 deduced from the DNA sequence is shown in the sequence ID No. 4.

As generally known in this art, the amino acid sequence shown in the Sequence ID No. 4 has a signal peptide. Therefore, the protein of the present invention may be the whole Sequence ID No. 4, a portion of the sequence (for example, the Sequence ID No. 4 except the sequence of a signal peptide), or the portion of the Sequence together with a linker.

40 The protein of the present invention includes at least an active portion having an activity to enhance the growth of vascular endothelial cells obtainable from a nucleotide sequence or a portion of the nucleotide sequence represented by the Sequence ID No. 5. The DNA corresponding to the signal peptide in the nucleotide sequence represented by the Sequence ID No. 5 may be changed another DNA corresponding to another signal peptide, if necessary, a signal peptide together with a linker DNA sequence may be used in the DNA fragment represented by the Sequence ID No. 5 attached hereto.

45 **Example 2 Affinity for concanavalin A**

The highly purified product obtained in the step (4) of Example 1 was checked for its affinity for concanavalin A in accordance with the procedure described in the foregoing. As the results, it was confirmed that the purified product was possessed of the affinity for concanavalin A, which is a

In addition, on the basis of the results obtained in Examples 1 and 2, it was confirmed that the high purity product of the step (4) was a single chain glycoprotein.

50 **Example 3 New formation of blood vessels**

A total of 10 avian eggs, fertilized for 8 days, were used in each test group. A filter (6 mm in diameter) which has been impregnated with a varied amount of the highly purified product (glycoprotein of this invention) ob-

tained in the step (4) of Example 1 was put on the chorio-allantoic membrane of each egg. After 3 days of incubation at 37°C under a moist condition, new formation of blood vessels was observed under a stereoscopic microscope. The judgement was made as positive (+, new formation of blood vessels around the filter) or negative (-, no formation of new blood vessels), and the number of positive eggs in each test group was counted. As a comparative example, the same experiment was carried out except that the filter was impregnated with physiological saline instead of the purified product. The results are shown in Table 1.

Table 1

Test group	Amount of glycoprotein	Positive eggs/Total
1	0 (physiological saline)	0/10
2	1 ng/filter	1/10
3	10 ng/filter	3/10
4	50 ng/filter	5/10
5	100 ng/filter	6/10

It is evident from the above table that the glycoprotein of the present invention is possessed of a function to enhance new formation of blood vessels.

Example 4 Growth enhancing effect on human umbilical cord vascular endothelial cells

Human umbilical cord vascular endothelial cells were prepared in the usual way and inoculated into a collagen-coated 24 well multi-dish (Corning Glassworks) with a cell density of 1×10^4 cells/well, using MCDB107 medium (Kyokuto Pharmaceutical Industrial Co., Ltd.) supplemented with 20% fetal calf serum. At intervals of 2 days from the next day, the medium was exchanged for a fresh medium containing 5% fetal calf serum and a predetermined amount (see Table 2) of the glycoprotein of the present invention obtained in the step (4) of Example 1. The number of cells was counted on the eighth day, with the results shown in Table 2.

Table 2

Glycoprotein (ng/ml)	Cell count (cells/well)
0	27168
0.3	29460
1.0	30920
3.3	37492
10.0	43072
33.3	54772
100.0	53988
333	46460

As is evident from the above table, the glycoprotein of the present invention is possessed of a function to enhance the growth of human umbilical cord vascular endothelial cells.

Example 5 Presence/absence examination of growth enhancing effect on fibroblasts

A primary culture of human dermis fibroblasts prepared from human skin was subcultured, and the eighth subculture was inoculated into a 24 well multi-dish with a cell density of 5×10^3 cells/well, using DME medium (Flow Laboratories, Inc.) supplemented with 10% fetal calf serum. At intervals of 2 days from the next day, the medium was exchanged for fresh DME medium containing 0.5% fetal calf serum and 100 ng/ml of the glycoprotein of the present invention obtained in the step (4) of Example 1.

As a comparative example, the same procedure was repeated except that the glycoprotein was eliminated

from the medium or a basic fibroblast growth factor (bFGF) was used in an amount of 1 ng/ml instead of the glycoprotein.

The number of cells was counted on the eighth day, with the results shown in Table 3.

Table 3

Component added	Cell count on 8th day (cells/well)
No addition	28248
Glycoprotein of Example 1	24325
bFGF	42645

As is evident from the above table, bFGF strongly enhances the growth of fibroblasts, but the number of fibroblasts on the eighth day in the case of the addition of the glycoprotein of the present invention obtained in Example 1 is almost the same as that of the case of the control (no addition), thus showing that the inventive glycoprotein hardly has a function to enhance the growth of fibroblasts.

Example 6 Presence/absence examination of growth enhancing effect on vascular smooth muscle cells

A primary culture of human smooth muscle cells prepared from an umbilical cord was subcultured, and the sixth subculture was inoculated into a 24 well multi-dish with a cell density of 5×10^3 cells/well, using DME medium supplemented with 10% fetal calf serum. At intervals of 2 days from the next day, the medium was exchanged for fresh medium containing 100 ng/ml of the glycoprotein of the present invention obtained in step (4) of Example 1.

As a comparative example, the same procedure was repeated except that the glycoprotein was eliminated from the medium or a basic fibroblast growth factor (bFGF) was used in an amount of 1 ng/ml instead of the glycoprotein.

The number of cells was counted on the eighth day, with the results shown in Table 4.

Table 4

Component added	Cell count on 8th day (cells/well)
No addition	6192
Glycoprotein of Example 1	7480
bFGF	48962

As is evident from the above table, the number of smooth muscle cells on the eighth day in the case of the addition of the glycoprotein of the present invention obtained in Example 1 is almost the same as that of the case of the control (no addition), thus showing that the inventive glycoprotein has no activity to enhance the growth of human smooth muscle cells.

Example 7 Presence/absence examination of growth enhancing effect on hepatocytes

Hepatic parenchymal cells (to be referred to as "hepatocytes" hereinafter) were prepared in accordance with the procedure of Takahashi et al. (*Tissue Culture*, vol.12, No.8, pp.308 - 312, 1986). The thus prepared hepatocytes were suspended in an inoculation medium (WE basal medium supplemented with 5% fetal calf serum and 10^{-6} M dexamethasone) to a cell density of 5.0×10^4 cells/0.2 ml, and the resulting hepatocyte suspension was inoculated into a collagen-coated 24 well multi-dish. After 4 hours of the culturing, the medium was replaced by WE basal medium and the glycoprotein of the present invention obtained in Example 1 was added to the fresh medium in a predetermined amount as shown in Table 5. The same process was repeated after additional 16 hours of the culturing. The medium was exchanged again for fresh WE basal medium 40 hours after the commencement of the culturing, and ^3H -thymidine was added to the fresh medium to carry out 2 hours of pulse-labeling. After completion of the pulse-labeling, the culture supernatant was removed, and the remaining cells were washed with a cold phosphate buffer (PBS), 2% perchlorate and 95% cold ethanol in that order and then dried at room temperature. In this instance, each washing step was repeated three times. The thus dried cells in each well were lysed by adding 0.8 ml of a 1% SDS/0.1 N NaOH solution and maintaining

the mixture at 37°C for at least 1 hour. A 0.5 ml portion of the resulting lysate was pipetted off from each well and put into a scintillation vial. Thereafter, the content in the vial was mixed with 7 ml of a scintillator (OptiFlow, Packard), and the radioactivity was measured using a scintillation counter to examine ^{3}H -thymidine uptake.

As a comparative example, the same experiment was carried out except that a mixture of insulin (100 nM/ml) and epidermal growth factor (EGF, 50 ng/ml) was used instead of the glycoprotein of the present invention.

The results are shown in Table 5.

Table 5

Component added	Uptake of ^{3}H -thymidine
<u>Glycoprotein of Example 1</u>	
300 ng/ml	5697 DPM
100 ng/ml	4347 DPM
30 ng/ml	4869 DPM
10 ng/ml	4619 DPM
<u>Insulin + EGF</u>	
(100 nM + 50 ng/ml)	76815 DPM
Control (no addition)	4992 DPM

As is evident from the above table, uptake of ^{3}H -thymidine does not occur by the addition of the glycoprotein of the present invention, thus showing that the inventive glycoprotein has no activity to enhance the growth of hepatocytes.

Example 8 Presence/absence examination of growth enhancing or inhibiting effect on HeLa cells

HeLa-S3 cells were suspended in MEM medium containing 5% bovine serum to a cell density of 1×10^6 cells/ml. The thus prepared HeLa-S3 cell suspension was dispensed in 100 μ l portions into wells of a 96 well multi-dish. After 24 hours of culturing, the resulting medium was replaced by fresh MEM medium which has been supplemented with 5% fetal calf serum and a predetermined amount of the glycoprotein obtained in Example 1, and the culturing was continued for additional 48 hours.

Since the presence or absence of the growth inhibiting effect was not able to be judged clearly with the naked eye under a phase-contrast microscope, the judgement was made by staining the cells with Crystal Violet. That is, each well of the dish after the culturing was washed with a phosphate buffer and then filled with a 10% formalin solution for a period of 30 minutes to fix the cells. The thus treated dish was dried after washing it with running water to remove formalin, and the cells in the dish were stained for 15 minutes with a 0.2% Crystal Violet solution containing 2% ethanol. After removing unbound pigment by washing the dish in running water, and subsequently drying the dish, a predetermined amount of 1% sodium dodecyl sulfate solution was added to each well to dissolve the bound pigment. Thereafter, absorbance of the thus dissolved Crystal Violet was measured at a wave length of 540 nm.

As a control, the same culturing step was repeated except that the glycoprotein was not used, and the Crystal Violet staining and absorbance measurement at 540 nm were carried out in the same manner.

The results are shown in Table 6 in which the absorbance of the control at 540 nm is expressed as 1.00.

Table 6

Component added	Ratio of absorbance at 540 nm
<u>Glycoprotein of Example 1</u>	
300 ng/ml	1.02
100 ng/ml	1.01
30 ng/ml	1.01
10 ng/ml	1.02
Control (no addition)	1.00

As shown in the above table, the absorbance at 540 nm hardly changed by the addition of the glycoprotein of the present invention in comparison with the case of the control (no addition), thus confirming that the inventive glycoprotein has no activity to enhance or inhibit the growth of HeLa cells.

Example 9 Migration-stimulating activity on vascular endothelial cells and smooth muscle cells

Primary culturing of vascular endothelial cells was carried out by isolating the cells from rabbit cornea capillary vessels in the usual way. The migration-stimulating activity of the cells was measured in accordance with the Boyden's test using Boyden's chamber. That is, DME medium supplemented with 10% fetal calf serum and a predetermined amount of the glycoprotein obtained in Example 1 was put into the lower compartment of the Boyden's chamber, and another DME medium supplemented with 10% fetal calf serum and 2×10^4 /ml of vascular endothelial cells was put into the upper compartment of the chamber. Thereafter, culturing was carried out at 37°C for 4 hours.

A similar test was carried out using primary-cultured smooth muscle cells which have been isolated from rat pulmonary artery.

After the culturing, the thus treated cells were stained with Diff-Quick solution, and the number of migrated cells per visual field was counted under a microscope, with the results shown in Table 7.

Table 7

	The number of migrated cells	
Glycoprotein	Vascular endothelial cells	Smooth muscle cells
300 ng/ml	268	0
100 ng/ml	50	0
30 ng/ml	37	0

As is evident from the above table, the glycoprotein of the present invention shows migration-stimulating activity on vascular endothelial cells but not on smooth muscle cells.

Thus, it is apparent that there has been provided, in accordance with the present invention, a novel protein of human origin, as well as a process for the production thereof. Since the protein of the present invention enhances the growth of vascular endothelial cells but does not activate the growth of smooth muscle cells, fibroblasts and hepatocytes and also does not enhance or inhibit the growth of HeLa cells, it can enhance the growth of vascular endothelial cells selectively and therefore can enhance new formation of blood vessels smoothly without causing secondary reactions. Because of such excellent properties, especially its activity to enhance new formation of blood vessels, the protein of the present invention can be applied to a healing enhancer of wound, burn injury, decubitus, postoperative tissue damage or the like or as a drug for the treatment of cardiac angiopathy, as well as its application to artificial organs such as artificial blood vessel, artificial skin and the like. It also can be applied to diagnostic and therapeutic drugs of malignant tumor, retinopathy, chronic rheumatoid arthritis and the like.

In addition, the protein of the present invention can be obtained with a high productivity and a high purity in comparison with the prior art physiologically active factors.

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

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(C) CITY: TOKYO
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(F) POSTAL CODE (ZIP): 151

10 (ii) TITLE OF INVENTION: Novel protein of human origin and its
production process

20 (iii) NUMBER OF SEQUENCES: 7

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

30 (v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 92 403 199.0

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 3-337999
(B) FILING DATE: 28-NOV-1991

35 (2) INFORMATION FOR SEQ ID NO: 1:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

50 (v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
(G) CELL TYPE: Ovarian
(H) CELL LINE: HUOCA II / HUOCA III

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

5 Arg Asn Thr Ile His Glu Phe
1 5

(2) INFORMATION FOR SEQ ID NO: 2:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

20 (iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

25 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(G) CELL TYPE: Ovarian
(H) CELL LINE: HUOCA II / HUOCA III

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Glu Phe Gly His Glu Phe Asp Leu Tyr Glu
1 5 10

35 (2) INFORMATION FOR SEQ ID NO: 3:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

50 (v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(G) CELL TYPE: Ovarian
(H) CELL LINE: HUOCA II / HUOCA III

(ix) FEATURE:

5 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /label= Xaa
 /note= "unidentified amino acid residue"

(ix) FEATURE:

10 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /label= Xaa
 15 /note= "unidentified amino acid residue"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

20 Glu Ser Xaa Val Leu Thr Ala Arg Gln Xaa Phe Pro Ser Arg Asp Leu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 4:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 728 amino acids
 (B) TYPE: amino acid
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (G) CELL TYPE: ovarian
 40 (H) CELL LINE: HUOCA II / HUOCA III

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

45 Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Gln His Val Leu
 1 5 10 15
 50 Leu His Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
 20 25 30
 Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
 35 40 45

Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
 50 55 60
 5 Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
 65 70 75 80
 Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
 10 85 90 95
 100 105 110
 Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
 115 120 125
 Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
 15 130 135 140
 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
 145 150 155 160
 Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
 20 165 170 175
 Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr
 180 185 190
 25 Cys Arg Asn Pro Arg Gly Glu Glu Gly Pro Trp Cys Phe Thr Ser
 195 200 205
 Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu
 30 210 215 220
 Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp
 225 230 235 240
 His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro
 35 245 250 255
 His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp
 260 265 270
 40 Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr
 275 280 285
 Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys
 45 290 295 300
 Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu
 305 310 315 320
 Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu
 325 330 335
 50 His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn
 340 345 350

Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr
 355 360 365
 5 Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp
 370 375 380
 Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met
 385 390 395 400
 10 Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp
 405 410 415
 Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala
 15 420 425 430
 Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His
 435 440 445
 20 Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys
 450 455 460
 Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu
 465 470 475 480
 25 Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val
 485 490 495
 Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg
 30 500 505 510
 Tyr Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp
 515 520 525
 Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr
 35 530 535 540
 545 550 555 560
 40 Cys Lys Gln Val Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly
 565 570 575
 Ser Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp
 45 580 585 590
 Phe Val Ser Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu
 595 600 605
 Lys Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn
 50 610 615 620
 Tyr Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu
 625 630 635 640
 55 Lys Cys Ser Gln His His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu
 645 650 655

5 Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp
 660 665 670
 Tyr Gly Gly Pro Leu Val Cys Glu Gin His Lys Met Arg Met Val Leu
 675 680 685
 10 Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly
 690 695 700
 Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile
 705 710 715 720
 15 Leu Thr Tyr Lys Val Pro Gln Ser
 725

(2) INFORMATION FOR SEQ ID NO: 5:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2187 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGGGGTGA	CCAAACTCT	GGCAGGCTC	CTGCTCAGC	ATGTCCTCCT	GCATCTCTC	60
CTGCTCCCCA	TCCGCATCC	CTATGCAAG	GGACAAAGGA	AAAAGAAAAA	TACAATTGAT	120
GAATTCAAA	AATCAGCAA	GACTACCTA	ATCAAATAG	ATCCAGCACT	QAAGATAAAA	180
ACCAAAAGAAG	TGAATTCG	AGACCAATGT	GCTAAATAGAT	GTACTAGGAA	TAAGGACTT	240
CCATTCACT	GCAGGGCTT	TGTGTTGAT	AAACGAAGAA	ACAAATGCC	CTGGTTCCCC	300
TTCAATAGCA	TGTCAGTGG	ATGCAAAAAAA	GAATTTCGCC	ATGAATTGAG	CCCTCTATGAA	360
AACAAAGACT	ACATTAAGAA	CTGCATCAT	GTTAAAGGAC	GGAGCTACAA	GGGAACAGTA	420
TCTATCACTA	AGAGTGCAT	CAAAATGCG	CCCTGGAGTT	CCATGATACC	ACACAAACAC	480
ACGTTTTCG	CTTCGAGCTA	TGGGGCTAA	GACCTACAGG	AAAACTACTG	TGCAAATCTC	540
CGAGGGGAAAG	AAGGGGGACC	CTGGTGTTC	ACAAGCAATC	CAGAGGTAGC	CTACGAAGTC	600
TGTGACATTC	CTCAGTGTG	AGAAAGTGTAA	TCATGACCT	CCAAATGGGG	GACTTATCGA	660
GGTCTCATGG	ATCATACAGA	ATCAGGCAAG	ATTTGTCAGC	CTGGGGATCA	TCAGACACCA	720
CACCCGACAA	AATTCTTCG	TGAAAGATAT	CCCGACAAAGG	GCTTGTGATG	TAATTATTCG	780
CCGAACTCCC	ATGGCCGACG	GAGGCCATGG	TGCTATACCT	TTGACCCCTCA	CACCCGCTGG	840
GAGTACTGTG	CAATTAACAC	ATGCGCTGAC	AATACACTTG	ATGACACTGA	TGTTCTCTTG	900
GAACAACTG	AATGCACTCA	AGGTCAAGGA	GAAGGCTACAA	GGGGCAGCTGT	CAATACATT	960
TGGAATGAA	TTCCATGTCA	GGCITGGGAT	TCTCAGTATC	CTCACGACAA	TGACATGACT	1020

5	CCTGAAATT TCAAGTCAA GGACCTACGA GAAAATTACT GCCGAAATCC AGATGGTCT	1080
	GAATCACCT GTGTTTAC CACTGATCCA AACATCCGAG TTGGCTACTG CTCCCAAATT	1140
	CCAAACTCTG ATATGTCACA TGGACAAGAT TTGTTATCCCTG GGAATGGCAA AAATTATATG	1200
	GGCAACTTAT CCCAAACAAAG ATCTGGACTA ATAGTCAA TGTGGACAA GAACATGGAA	1260
	GACTTACATC GTCATATCTT CTGGGAAACCA CATGCAAGTA ACCTGAATGA GAATTACTGC	1320
10	CGAAATCCAG ATGATGATCC TCATGGACCC TTGTGCTACA CGGGAATCC ACTCAATTCT	1380
	TOGGATTATTG GCCTATTTCG TGTTGTCGAA CGTGTACCC CACCTAACAT AGTCAATTTA	1440
	GACCATCCCG TAATATCTG TGCCAAACACG AAACAATTCG GAGITGTAAGA TGCGGATTCGA	1500
	ACACCAACAA ACATAGATG GATGTTAGT TTGAGATACA GAATAAAACA TATCTCGGGA	1560
	GGATCATGTA TAAAGGAGAG TTGGGTTGATC ACTGCACAC AGTGTTCCTC TTCTCGAGAC	1620
15	TTGAAAGATT ATGAAAGCTT GCTTGGAAATT CATGATGGCC ACAGGAAGAGG AGATGAGAAA	1680
	TGCAACACGG TTCTCAATG TTCCAGCTG GTATATGGCC CTGAAAGGATC AGATCTGGT	1740
	TTAATGAAGC TTGCGAGGC TCTGTCTCG OATGATTTTG TTAGTACGAT TGATTTACCT	1800
	AATTATGGAT CCACAAATTCG TGAAAAGACCC AGTGGAGCTG TTATGGCTG GGCTCACACT	1860
20	GGATGTCGA ACTATGATGG CCTTATTCGA CTGGCACATC TCTATATAAT GGGAAATGAG	1920
	AAATGCAGCC AGCATCATCG AGGGAAAGGTG ACTCTGAATG AGTCTGAAT ATGTCGGG	1980
	GCTGAAAAGA TTGGATCAGG ACCATGTGAG GGGGATTATG GTGCCCAACT TGTTTGTGAG	2040
	CAACATAAA TGAAATGTT TCTTGTGTCG ATTTGTCCTG GTCTGGATG TGCCATTCCA	2100
	AATCGTCCTG GTATTTTGTG CCGAGTACCA TATTATGCAA AATGGATACA CAAAATTATT	2160
25	TTAACATATA AGGTACCCACA GTCTAG	2187

(2) INFORMATION FOR SEQ ID NO: 6:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 2576 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
35	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: mRNA
40	(iii) HYPOTHETICAL: YES
	(iii) ANTI-SENSE: NO
45	(ix) FEATURE:
	(A) NAME/KEY: CDS
	(B) LOCATION: join(102..2285, 2289..2294, 2298..2336, 2340
	..2384, 2388..2480, 2484..2507, 2514..2522, 2526
	..2570)
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGGUCAGAG CGGACUGGGCU CUUUUAGGCA CUGACUCCGA ACAGGAUUCU UUCACCCAGG 60

5	CAUCUCCUCC AGAGGGAUCC GCGAGCCCCU CCAGCAGCAC C AUG UGG GUG ACC	113
	Met Trp Val Thr	
	1	
10	AAA CUC CUG CCA GCC CUG CUG CAG CAU GUC CUC CUQ CAU CUC CUC Lys Leu Leu Pro Ala Leu Leu Leu Glu His Val Leu Leu His Leu Leu 5 10 15 20	161
15	CUG CUC CCC AUC GCC AUC CCC UAU GCA GAG GGA CAA AGG AAA AGA AGA Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Glu Arg Lys Arg Arg 25 30 35	209
20	AAU ACA AUU CAU GAA UUC AAA AAA UCA GCA AAG ACU ACC CUA AUC AAA Asn Thr Ile His Glu Phe Lys Ser Ala Lys Thr Thr Leu Ile Lys 40 45 50	257
25	AUA GAU CCA GCA CUG AAG AUA AAA ACC AAA AAA GUG AAU ACU GCA GAC Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Val Asn Thr Ala Asp 55 60 65	305
30	CAA UGU GCU AAU AGA UGU ACU AGG AAU AAA GGA CUU CCA UUC ACU UGC Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Glu Leu Pro Phe Thr Cys 70 75 80	353
35	AAG GCU UUU GUU UUU GAU AAA GCA AGA AAA CAA UGC CUC UGG UUC CCC Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Glu Cys Leu Trp Phe Pro 85 90 95 100	401
40	UUC AAU AGC AUG UCA AQU GGA GUG AAA AAA GAA UUU GGC CAU GAA UUU Phe Asn Ser Met Ser Ser Gly Val Lys Glu Phe Gly His Glu Phe 105 110 115	449
45	GAC CUC UAU GAA AAC AAA GAC UAC AUU AGA AAC UGC AUC AUC UGU AAA Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys Ile Ile Gly Lys 120 125 130	497
50	GGA CGC AGC UAC AAG GGA ACA GUA UCU AUC ACU AAG AGU GGC AUC AAA Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys Ser Gly Ile Lys 135 140 145	545
	UGU CAG CCC UGG AGU UCC AUG AUA CCA CAC GAA CAC AGC UUU UUG CCU Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His Ser Phe Leu Pro 150 155 160	593

5	UCG AGC UAU CGG GGU AAA GAC CUA CAG GAA AAC UAC UGU CGA AAU CCU Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro 165 170 175 180	641
10	CGA GGG GAA GAA GGG GGA CCC UGG UGU UUC ACA AGC AAU CCA GAG GUA Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val 185 190 195	689
15	CGC UAC GAA GUC UGU GAC AUU CCU CAG UGU UCA GAA GUU GAA UGC AUG Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met 200 205 210	737
20	ACC UCC AAU GGG GAG AGU UAU CGA GGU CUC AUG GAU CAU ACA GAA UCA Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser 215 220 225	785
25	GGC AGC AAU UGU CAG CGC UGG GAU CAU CAG ACA CCA CAC CGG CAC AAA Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys 230 235 240	833
30	UUC UUG CCU GAA AGA UAU CCC GAC AAG GGC UUU GAU GAU AAU UAU UGC Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys 245 250 255 260	881
35	CGC AAU CCC GAU GGC CAG CCG AGG CCA UGG UGC UAU ACU CUU GAC CCU Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro 265 270 275	929
40	CAC ACC CGC UGG GAG UAC UGU GCA AAU AAA ACA UGC GCU GAC AAU ACU His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr 280 285 290	977
45	AUG AAU GAC ACU GAU GUU CCU UUG GAA ACA ACU GAA UGC AUC CAA GGU Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly 295 300 305	1025
50	CAA GGA GAA GGC UAC AGG GGC ACU GUC AAU ACC AAU UGG AAU GGA AAU Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile 310 315 320	1073
55	CCA UGU CAG CGU UGG GAU UCU CAG UAU CCU CAC GAG CAU GAC AUG ACU Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr 325 330 335 340	1121

5	CCU GAA AAU UUC AAG UGC AAG GAC CUA CGA GAA AAU UAC UGC CGA AAU Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn 345 350 355	1169
10	CCA GAU GGG UCU GAA UCA CCC UGG UGU UUU ACC ACU GAU CCA AAC AUC Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile 360 365 370	1217
15	CGA GUU GGC UAC UGC UCC CAA AAU CCA AAC UGU GAU AUG UCA CAU CGA Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly 375 380 385	1265
20	CAA GAU UGU UAU CGU GGG AAU GGC AAA AAU UAU AUG GGC AAC UUA UCC Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser 390 395 400	1313
25	CAA ACA AGA UCU GGA CUA ACA UGU UCA AUG UGG GAC AAG AAC AUG GAA Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu 405 410 415 420	1361
30	GAC UUA CAU CGU CAU AUC UUC UGG GAA CCA GAU GCA AGU AAG CUG AAU Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn 425 430 435	1409
35	GAG AAU UAC UGC CGA AAU CCA GAU GAU GCU CAU GGA CCC UGG UGC Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His Gly Pro Trp Cys 440 445 450	1457
40	UAC ACG GGA AAU CCA CUC AAU CGU UGG GAU UAU UGC CCU AAU UCU CGU Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg 455 460 465	1505
45	UGU GAA GGU GAU ACC ACA ACA AAU GUC AAU UUA GAC CAU CCC GUA Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp His Pro Val 470 475 480	1553
50	AUA UCU UGU GCC AAA ACG AAA CAA UUG CGA GUU GUA AAU GGG AGU CCA Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val Asn Gly Ile Pro 485 490 495 500	1601
55	ACA CGA ACA AAC AAU GGA UGG AUG GUU AGU UUG AGA UAC ACA AAU AAA Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr Arg Asn Lys 505 510 515	1649

5	CAU AUC UGC GGA GGA UCA UUG AUA AAG GAG AGU UGG QUU CUU ACU GCA His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val Leu Thr Ala	1697
	520 525 530	
10	CGA CAG UGU UUC CCU UCU CGA GAC UUG AAA GAU UAU GAA GCU UGG CUU Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp Leu	1745
	535 540 545	
15	GGA AUU CAU GAU GUC CAC GGA AGA GGA GAU GAG AAA UGC AAA CAG GUU Gly Ile His Asp Val His Gly Arg Gly Asp Glu Lys Cys Lys Gln Val	1793
	550 555 560	
20	CUC AAU GUU UCC CAG CUG GUA UAU GGC CCU GAA GGA UCA GAU CUG GUU Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly Ser Asp Leu Val	1841
	565 570 575 580	
25	UUA AUG AAG CUU GCC AGG CCU GCU GUC CUG GAU GAU UUU GUU AGU ACG Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp Phe Val Ser Thr	1889
	585 590 595	
30	AUU GAU UUA CCU AAU UAU GGA UGC ACA AAU CCU GAA AAG ACC AGU UGC Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu Lys Thr Ser Cys	1937
	600 605 610	
35	AGU GUU UAU GGC UGG GGC UAC ACU GGA UUG AUC AAC UAU GAU GGC CUA Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr Asp Gly Leu	1985
	615 620 625	
40	UUA CGA CGC GCA CAU CUC UAU AUA AUG GCA AAU GAG AAA UCC AGC CAG Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys Cys Ser Gln	2033
	630 635 640	
45	CAU CAU CGA CGG AAG GUG ACU CUG AAU GAG UCU GAA AUA UGU GCU CGG His His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu Ile Cys Ala Gly	2081
	645 650 655 660	
50	GCU GAA AAG AUU GGA UCA CGA CCA UGU GAG CGG GAU UAU GGU GGC CCA Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr Gly Pro	2129
	665 670 675	
	CUU GUU UGU GAG CAA CAU AAA AUG AGA AUG GUU CUU CGU GUC AUU GUU Leu Val Cys Glu Gln His Lys Met Arg Met Val Leu Gly Val Ile Val	2177
	680 685 690	

5	CCU GGU CGU GGA UGU GCC AUU CCA AAU CGU CCU GGU AUU UUU GUC CGA Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile Phe Val Arg 695 700 705	2225
10	GUA GCA UAU UAU GCA AAA UGG AUA CAC AAA AUU AUU UUA ACA UAU AAG Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile Leu Thr Tyr Lys 710 715 720	2273
15	GUA CCA CAG UCA UAG CUG AAG UAA GUG UGU CUG AAG CAC CCA CCA AUA Val Pro Gln Ser Leu Lys Val Cys Leu Lys His Pro Pro Ile 725 730 735	2321
20	CAA CUG UCU UUU ACA UGA AGA UUU CAG AGA AUG UGG AAU UUA AAA UGU Gln Leu Ser Phe Thr Arg Phe Gln Arg Met Trp Asn Leu Lys Cys 740 745 750	2369
25	CAC UUA CAA CAA UCC UAA GAC AAC UAC UGG AGA GUC AUG UUU GUU GAA His Leu Gln Gln Ser Asp Asn Tyr Trp Arg Val Met Phe Val Glu 755 760 765	2417
30	AUU CUC AUU AAU GUU UAU GGG UGU UUU CUG UUG UUU UGU UUG UCA GUG Ile Leu Ile Asn Val Tyr Gly Cys Phe Leu Leu Phe Cys Leu Ser Val 770 775 780	2465
35	UUA UUU UGU CAA UGU UGA AGU GAA UUA AGG UAC AUG CAA GUG Leu Phe Cys Gln Cys Ser Glu Leu Arg Tyr Met Gln Val 785 790 795	2507
40	UAAUAA CAU AUC UCC UGA AGA UAC UUG AAU GGA UUA AAA AAA CAC ACA His Ile Ser Arg Tyr Leu Asn Gly Leu Lys Lys His Thr 800 805 810	2555
45	GGU AUA UUU GCU GGA UGAUAA Gly Ile Phe Ala Gly 815	2576

45 (2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 815 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

5 Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu
 1 5 10 15
 Leu His Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
 20 25 30
 10 Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
 35 40 45
 Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
 15 50 55 60
 16 Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
 65 70 75 80
 20 Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
 85 90 95
 25 Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
 100 105 110
 30 Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
 115 120 125
 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
 130 135 140
 35 Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
 145 150 155 160
 Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr
 165 170 175
 40 Cys Arg Asn Pro Arg Gly Glu Glu Gly Pro Trp Cys Phe Thr Ser
 180 185 190
 Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu
 195 200 205
 45 Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp
 210 215 220
 His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro
 225 230 235 240
 His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp
 245 250 255
 50 Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr
 260 265 270
 55 Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys
 275 280 285

Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu
 290 295 300
 5 Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile
 305 310 315 320
 Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu
 325 330 335
 10 His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn
 340 345 350
 Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr
 15 355 360 365
 Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp
 370 375 380
 20 Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met
 385 390 395 400
 Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp
 405 410 415
 25 Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala
 420 425 430
 Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His
 30 435 440 445
 Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys
 450 455 460
 35 Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu
 465 470 475 480
 Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val
 485 490 495
 40 Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg
 500 505 510
 Tyr Arg Asn Lys His Ile Cys Gly Ser Leu Ile Lys Glu Ser Trp
 515 520 525
 45 Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr
 530 535 540
 Glu Ala Trp Leu Gly Ile His Asp Val His Gly Arg Gly Asp Glu Lys
 545 550 555 560
 50 Cys Lys Gln Val Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly
 565 570 575
 55 Ser Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp
 580 585 590

Phe Val Ser Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu
 595 600 605
 5 Lys Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn
 610 615 620
 Tyr Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu
 625 630 635 640
 10 Lys Cys Ser Gln His His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu
 645 650 655
 Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp
 15 660 665 670
 Tyr Gly Gly Pro Leu Val Cys Glu Gln His Lys Met Arg Met Val Leu
 675 680 685
 20 Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly
 690 695 700
 Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile
 705 710 715 720
 25 Leu Thr Tyr Lys Val Pro Gln Ser Leu Lys Val Cys Leu Lys His Pro
 725 730 735
 Pro Ile Gln Leu Ser Phe Thr Arg Phe Gln Arg Met Trp Asn Leu Lys
 30 740 745 750
 Cys His Leu Gln Gln Ser Asp Asn Tyr Trp Arg Val Met Phe Val Glu
 755 760 765
 35 Ile Leu Ile Asn Val Tyr Gly Cys Phe Leu Leu Phe Cys Leu Ser Val
 770 775 780
 Leu Phe Cys Gln Cys Ser Glu Leu Arg Tyr Met Gln Val His Ile Ser
 785 790 795 800
 40 Arg Tyr Leu Asn Gly Leu Lys Lys His Thr Gly Ile Phe Ala Gly
 805 810 815

45

50

55

Claims

5 1. A single chain protein selectively enhancing the growth of vascular endothelial cells, characterized in that
it comprises the following peptide chains :

(SEQ. ID No. : 1)

10 Arg Asn Thr Ile His Glu Phe

1 5

(SEQ. ID No. : 2)

Glu Phe Gly His Glu Phe Asp Leu Tyr Glu

15 1 5 10

(SEQ. ID No. : 3)

Glu Ser Xaa Val Leu Thr Ala Arg Gln Xaa Phe Pro Ser Arg Asp Leu

20 1 5 10 15

and in that it has a molecular weight of from 72,000 to 80,000 Da when determined by SDS polyacrylamide gel electrophoresis or from 79,000 to 85,000 Da when determined under reducing conditions.

25 2. A process for producing the protein according to claim 1 which comprises purifying a serum-free culture supernatant of said human ovarian tumor established cell line, HUOCA-II or HUOCA-III, by combining purification techniques including (a) cation exchange chromatography, (b) heparin affinity chromatography, (c) heparin affinity high performance liquid chromatography and (d) reverse phase high performance liquid chromatography.

30 3. A protein of human origin which contains an amino acid sequence or a portion of the amino acid sequence represented by the following sequence (SEQ ID No.: 4) :

35 Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val
1 10
Leu Leu His Leu Leu Leu Ieu Pro Ile Ala Ile Pro Tyr Ala Glu
20 30
Gly Gln Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser
40
40 Ala Lys Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys
50 60

45

50

Thr Lys Lys Val Asn Thr Ala Asp Gin Cys Ala Asn Arg Cys Thr
 70
 Arg Asn Lys Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp
 80 90
 5 Lys Ala Arg Lys Gin Cys Leu Trp Phe Pro Phe Asn Ser Met Ser
 100
 Ser Gly Val Lys Lys Glu Phe Gly His Glu Phe Asp Leu Tyr Glu
 110 120
 Asn Lys Asp Tyr Ile Arg Asn Cys Ile Ile Gly Lys Gly Arg Ser
 130
 10 Tyr Lys Gly Thr Val Ser Ile Thr Lys Ser Gly Ile Lys Cys Glu
 140 150
 Pro Trp Ser Ser Met Ile Pro His Glu His Ser Phe Leu Pro Ser
 160
 15 Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro
 170 180
 Arg Gly Glu Glu Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu
 190
 Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu
 200 210
 20 Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His
 220
 Thr Glu Ser Gly Ile Cys Gln Arg Trp Asp His Gln Thr Pro
 230 240
 His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe
 250
 25 Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp
 260 270
 Cys Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile
 280
 30 Lys Thr Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu
 290 300
 Glu Thr Thr Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly
 310
 35 Thr Val Asn Thr Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp
 320 330
 Ser Gln Tyr Pro His Glu His Asp Met Thr Pro Glu Asn Phe Lys
 340
 Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn Pro Asp Gly Ser
 350 360
 40 Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile Arg Val Gly
 370
 Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly Gln Asp
 380 390
 45 Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser Gln
 400
 Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu
 410 420
 Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu
 430
 50 Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His Gly Pro
 440 450
 Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro
 460

Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu
 470 480
 Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gin Leu Arg Val
 490
 5 Val Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser
 500 510
 Leu Arg Tyr Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys
 520
 10 Glu Ser Trp Val Leu Thr Ala Arg Glu Cys Phe Pro Ser Arg Asp
 530 540
 Leu Lys Asp Tyr Glu Ala Trp Leu Gly Ile His Asp Val His Gly
 550
 Arg Gly Asp Glu Lys Cys Lys Gln Val Leu Asn Val Ser Gln Leu
 560 570
 15 Val Tyr Gly Pro Glu Gly Ser Asp Leu Val Leu Met Lys Leu Ala
 580
 Arg Pro Ala Val Leu Asp Asp Phe Val Ser Thr Ile Asp Leu Pro
 590 600
 Asn Tyr Gly Cys Thr Ile Pro Glu Lys Thr Ser Cys Ser Val Tyr
 610
 20 Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr Asp Gly Leu Leu Arg
 620 630
 Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys Cys Ser Gln His
 640
 His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu Ile Cys Ala Gly
 650 660
 25 Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr Gly Gly
 670
 Pro Leu Val Cys Glu Gin His Lys Met Arg Met Val Leu Gly Val
 680 690
 30 Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile
 700
 Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile
 710 720
 Leu Thr Tyr Lys Val Pro Gin Ser 728

35

4. A pharmaceutical composition which contains the protein of claim 1 or 3 as an active ingredient.

5. A DNA fragment which contains a nucleotide sequence or a portion of the nucleotide sequence below
 40 (SEQ ID No.: 5):

ATG TGG GTG ACC AAA CTC CTG CCA GCC CTG CTG CTG CAG CAT
 1
 45 GTC CTC CTG CAT CTC CTC CTC CCC ATC GCC ATC CCC TAT
 GCA GAG GGA CAA AGG AAA AGA AGA AAT ACA ATT CAT GAA TTC
 93
 AAA AAA TCA GCA AAG ACT ACC CTA ATC AAA ATA GAT CCA GCA
 141
 50 CTG AAG ATA AAA ACC AAA AAA GTG AAT ACT GCA GAC CAA TGT
 189
 GCT AAT AGA TGT ACT AGG AAT AAA GGA CTT CCA TTC ACT TGC
 237

55

AAG GCT TTT GTT TTT GAT AAA GCA AGA AAA CAA TGC CTC TGG
 285
 TTC CCC TTC AAT AGC ATG TCA AGT GGA GTG AAA AAA GAA TTT
 322
 5 GGC CAT GAA TTT GAC CTC TAT GAA AAC AAA GAC TAC ATT AGA
 AAC TGC ATC ATT GGT AAA GGA CGC AGC TAC AAG GGA ACA GTC
 381
 TCT ATC ACT AAG AGT GGC ATC AAA TGT CAG CCC TGG AGT TCC
 429
 10 ATG ATA CCA CAC GAA CAC AGC TTT TTG CCT TCG AGC TAT CGG
 477
 GGT AAA GAC CTA CAG GAA AAC TAC TGT CGA AAT CCT CGA GGG
 525
 15 GAA GAA GGG GGA CCC TGG TGT TTC ACA AGC AAT CCA GAG GTC
 573
 CGC TAC GAA GTC TGT GAC ATT CCT CAG TGT TCA GAA CCT GAA
 621
 TGC ATG ACC TGC AAT GGG GAG AGT CAT CGA GGT CTC ATG GAT
 699
 20 CAT ACA GAA TCA GGC AAG ATT TGT CAG CGC TGG GAT CAT CAG
 ACA CCA CAC CGG CAC AAA TTC TTG CCT GAA AGA TAT CCC GAC
 717
 25 AAG GGC TTT GAT GAT AAT TAT TGC CGC AAT CCC GAT GGC CAG
 765
 CCG AGG CCA TGG TGC TAT ACT CTT GAC CCT CAC ACC CGC TGG
 813
 GAG TAC TGT GCA ATT AAA ACA TGC GGT GAC AAT ACT ATG AAT
 861
 30 GAC ACT GAT GTT CCT TTG GAA ACA ACT GAA TGC ATC CAA GGT
 909
 CAA GGA GAA GGC TAC AGG GGC ACT GTC AAT ACC ATT TGG AAT
 957
 GGA ATT CCA TGT CAG CGT TGG GAT TCT CAG TAT CCT CAC GAG
 1005
 35 CAT GAC ATG ACT CCT GAA AAT TTC AAG TGC AAG GAC CTA CGA
 GAA AAT TAC TGC CGA AAT CCA GAT GGG TCT GAA TCA CCC TGG
 1053
 40 TGT TTT ACC ACT GAT CCA AAC ATC CGA GTT GGC TAC TGC TCC
 1101
 CAA ATT CCA AAC TGT GAT ATG TCA CAT GGA CAA GAT TGT TAT
 1149
 CGT GGG AAT GGC ABA AAT TAT ATG GGC AAC TTA TCC CAA ACA
 1197
 45 AGA TCT GGA CTA ACA TGT TCA ATG TGG GAC AAG AAC ATG GAA
 1245
 GAC TTA CAT CGT CAT ATC TTC TGG GAA CCA GAT GCA AGT AAC
 1293
 CTG AAT GAG AAT TAC TGC CGA AAT CCA GAT GAT GAT GCT CAT
 1341
 50 GGA CCC TGG TGC TAC AGC GGA AAT CCA CTC ATT CCT TGG GAT
 TAT TGC CCT ATT TCT CGT TGT GAA GGT GAT ACC ACA CCT ACA
 1389
 55 ATA GTC AAT TTA GAC CAT CCC GTC ATA TCT TGT GCC AAA AGC
 1437
 AAA CAA TTG CGA GTT GTC AAT GGG ATT CCA ACA CGA ACA AAC
 1485

ATA GGA TGG ATG GTT AGT TTG AGA TAC AGA AAT AAA CAT ATC
 1533
 TGC GGA CGA TCA TTG ATA AAG GAG AGT TGG GTT CTT ACT GCA
 1581
 CGA CAG TGT TTC CCT TCT CGA CAC TTG AAA GAT TAT GAA GCT
 1629
 TGG CTT GGA ATT CAT GAT GTC CAC GGA AGA GGA GAT GAG AAA
 1677
 TGC AAA CAG GTT CTC AAT GTT TCC CAG CTG GTA TAT GGC CCT
 1725
 GAA GGA TCA GAT CTG GTT TTA ATG AAG CTT GCC AGG CCT GGT
 1773
 GTC CTG GAT GAT TTT GTT AGT ACG ATT GAT TTA CCT AAT TAT
 1821
 GGA TGC ACA ATT CCT GAA AAG ACC AGT TGC AGT GTT TAT GGC
 1869
 TGG GGC TAC ACT GGA TTG ATC AAC TAT GAT GGC CTA TTA CGA
 1917
 GTG GCA CAT CTC TAT ATA ATG GGA AAT GAG AAA TGC AGC CAG
 1965
 CAT CAT CGA GGG AAG GTG ACT CTG AAT GAG TCT GAA ATA TGT
 2013
 GCT GGG GCT GAA AAG ATT GGA TCA GGA CCA TGT GAG GGG GAT
 2061
 TAT GGT GGC CCA CTT GTT TGT GAG CAA CAT AAA ATG AGA ATG
 2109
 GTT CTT GGT GTC ATT GTT CCT GGT CGT GGA TGT GCC ATT CCA
 2157
 AAT CGT CCT GGT ATT TTT GTC CGA GTA GCA TAT TAT GCA AAA
 2187
 TGG ATA CAC AAA ATT ATT TTA ACA TAT AAG GTA CCA CAG TCA
 TAG
 wherein at least one base may be substituted based on the degeneracy of genetic code.

6. A single chain protein having an activity to enhance the growth of vascular endothelial cells obtainable from the DNA fragment of claim 5.
7. A DNA fragment complementary to the DNA fragment of claim 5.
8. An expression vector which contains the DNA fragment of claim 5.
9. A transformant transformed with the DNA fragment of claim 5.
10. A transformant transformed with the expression vector of claim 8.

FIG. 1

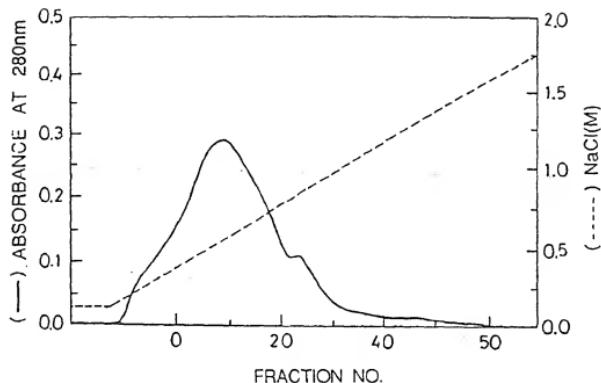


FIG. 2

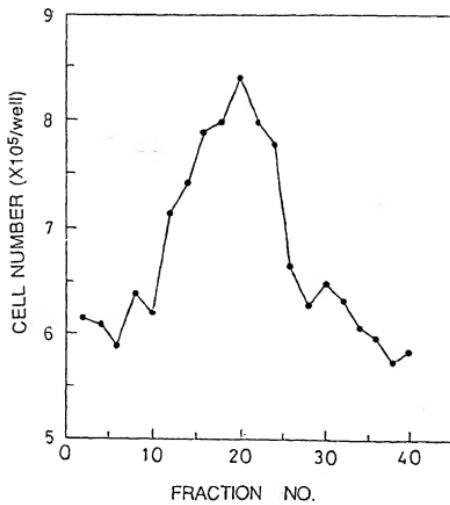


FIG. 3

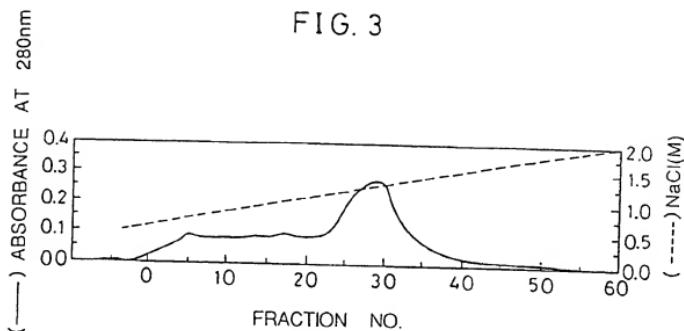


FIG. 4

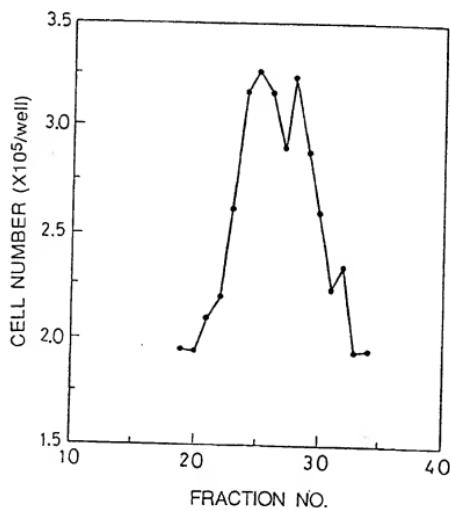


FIG.5

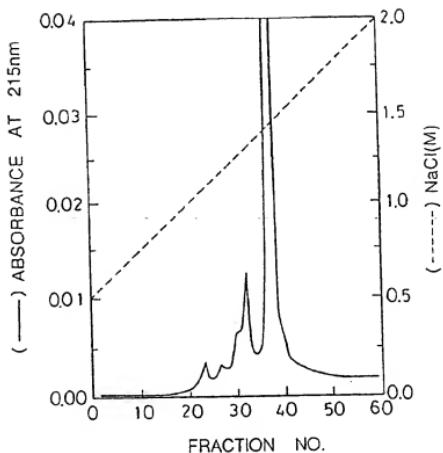


FIG.6

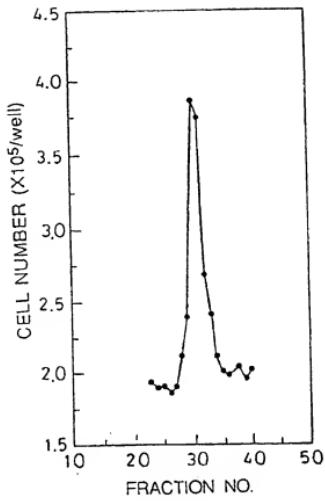


FIG. 7

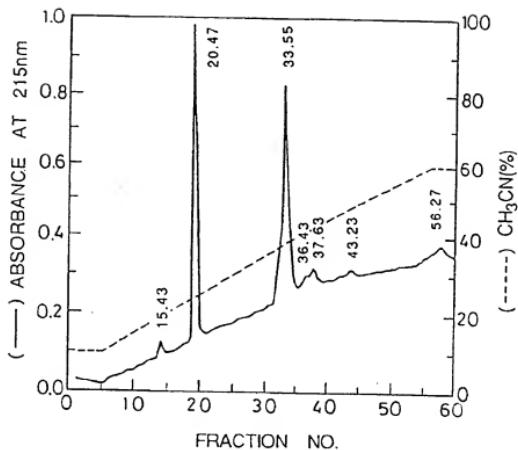


FIG. 8

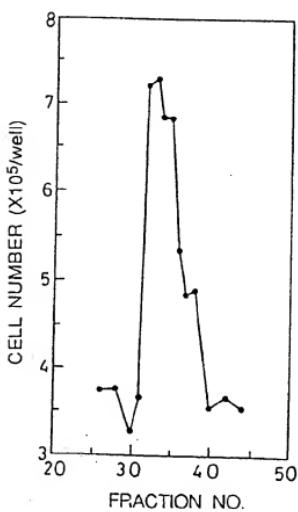


FIG. 9

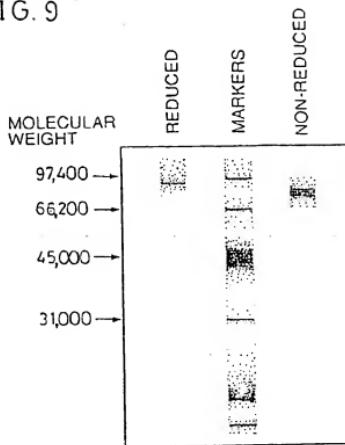


FIG. 10

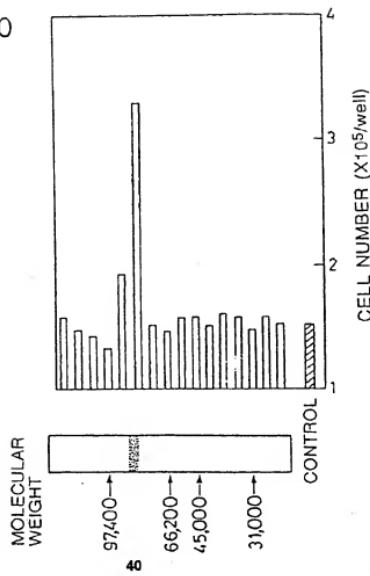


FIG. 11

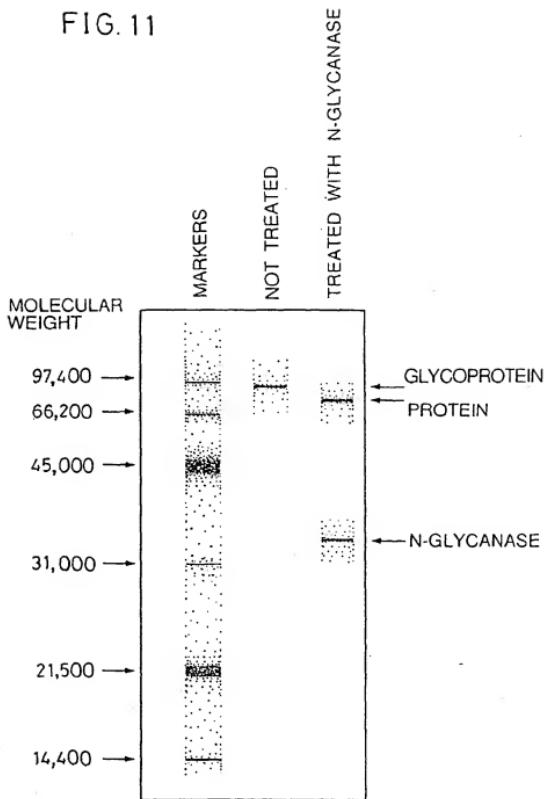


FIG. 12

1	GG GCU CAG AGC CGA CUG GCU CUU UUA GGC ACU GAC UCC GAA CAG GAU	4
48	UCU UUC ACC CAG GCA UCU CCU CCA GAG GGA UCC GCC AGC CCG UCC AGC	9
96	Met Trp Val Thr Lys Leu Ieu Pro Ala Leu Leu Leu Gln His	1
	GCG ACC AUG UGG GUG ACC AAA CUC CUG CCA GCC CUG CUG CAG CAU	14
15	Val Leu Leu His Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu	3
144	GUC CUC CUG CAU CUC CUC CUG CUC CCC AUC GCC AUC CCC UAU GCA GAG	19
31	Gly Gln Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala	4
192	GGA CAA CAG AAA GCA AAA ACA AUU CAU GAA UUC AAA AAA UCA GCA	23
47	Lys Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys	6
240	AAG ACU ACC CUA AUC AAA AUA GAU CCA GCA CUG AAG AUU AAA ACC AAA	28
83	Lys Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys	7
288	AAA GGU AAU ACU GCA GAC CAA UCU GCU AAU AGA UGU ACU AGG AAU AAA	33
79	Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys	9
336	GGA CUA CCA UUC ACU UGC AAC GGU UUU GGU UUU GAU AAA GCA AGA AAA	38
95	Gln Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys	11
384	CAA UGC CUC UGG UUC CCC UUC AAU AGC AUG UCA AGU GGA GUG AAA AAA	43
111	Glu Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg	12
432	GAA UUU GGC CAU GAA UUU GAC CUC UAU GAA AAC AAA GAC UAC AUU AGA	47
127	Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile	14
480	AAC UGC AUC AUU GGU AAA GGA CCC AGC UAC AAG GGA ACA GUA UCU AUC	52
143	Thr Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His	15
528	ACU AAG AGU GGC AUC AAA UGU CGC CCC UGG AGU UCC AUG AUU CCA CAC	57
159	Glu His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu	17
576	GAA CAC AGC UUU UUG CCU UCG AGC UAU CGG GGU AAA GAC CUA CAG GAA	62
175	Asn Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe	19
624	AAC UAC UGU CGA AAA CCU CGA GGG GAA GAA GGG GGA CCC UGG UGU UUC	67
191	Thr Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys	20
672	ACA AGC AAA CCA GAG GUA CGC UAC GAA GUC UGU GAC AUU CCU CAG UGU	71
207	Ser Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu	22
720	UCA GAA GUU GAA UGC AUG ACC UGC AAA GGG GAG AGU UAU CGA CGU CUC	76
223	Met Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln	23
788	AUG GAU CAU ACA GAA UCA GGC AAG AUU UGU CAG CGC CGC UGG GAU CAU CAG	81

FIG. 12 (cont.)

239	Thr Pro His Arg His Lys Phe Leu Pro Ciu Arg Tyr Pro Asp Lys Gly	25
816	ACA CCA CAC CGG CAC AAA UUC UUG CCU GAA AGA UAU CCC GAC AAG GGC	86
255	Phe Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp	27
864	UUU GAU GAU AAU UAU UGC CGC AAU CCC GAU GGC CAG CGG AGG CCA UGG	91
271	CYS Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys	28
912	UGC UAU ACU CUU GAC CCU CAC ACC CGC UGG GAG UAC UGU GCA AUU AAA	95
287	Thr Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr	30
960	ACA UGC GCU GAC AAU ACU AUG AAC GAC ACU GAU GUU CCU UUG GAA ACA	100
303	Thr Glu Cys Ile Gln Gly Glu Gly Glu Tyr Arg Gly Thr Val Asn	31
1008	ACU GAA UGC AUC CAA CGU CAA CGG GAA GGC UAC AGG GGC ACU GUC AAA	105
319	Thr Ile Trp Asn Gly Ile Pro Cys Glu Arg Trp Asp Ser Glu Tyr Pro	33
1056	ACC AUU UGG AAU GGA AUU CCA UGU CAG CGU UGG GAU UCU CAG UAU CCU	110
335	His Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg	35
1104	CAC GAG CAU GAC AUG ACU CCU GAA AAU UUC AAC UGC AAG GAC CUA CGA	115
351	Glu Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe	36
1152	GAA AAU UAC UGC CGA AAU CCA GAA UGG UCU GAA UCA CCC UGG UGU UUU	119
367	Thr Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn	38
1200	ACC GAC GAU CCA AAC AUC CGA GUU GGC UAC UGC UCC CAA AUU CCA AAC	124
383	Cys Asp Met Ser His Gly Glu Asp Cys Tyr Arg Gly Asn Gly Lys Asn	39
1248	UGU GAU AUG UCA CAU GGA CAA GAA UGU UAU CGU GGG AAU GGC AAA AAU	129
399	Tyr Met Gly Asn Leu Ser Glu Thr Arg Ser Gly Leu Thr Cys Ser Met	41
1296	UAU AUG GGC AAC UUA UCC CAA ACA AGA UCU GGA CUA ACA UGU UCA AUG	134
415	Trp Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro	43
1344	UGG GAC AAC AUG GAA GAC UUA CAU CGU CAA UAC UUC UGG GAA CCA	139
431	Asp Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp	44
1382	GAU GCA AGG AAC CGU AAU GAG AAU UAC UGC CGA AAU CCA GAU GAU	143
447	Ala His Gly Pro Trp Cys Tyr Thr Gly Asp Pro Leu Ile Pro Trp Asp	46
1440	GCU CAU GGA CCC UGG UGC UAC CGG GAA AAU CCA CUC AUU CCU UGG GAU	148
463	Tyr Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Tyr Ile Val	47
1488	UAU UGC CCU AAU UCU CGU UGU GAA GGU GAU ACC ACA CCU ACA AUA GUC	153
479	Asn Leu Asp His Pro Val Ile Ser Cys Ala Gly Lys Thr Lys Gln Leu Arg	49
1536	AAU AAA GAC CAU CCC GUA AAA UCU UGU CGC AAA ACG AAA CAA UUG CGA	158
495	Val Val Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser	51
1584	GUU GUA AAU GGG AAU CCA ACA CGA ACA AAC AUA GGA UGG AUG GUU AGU	163
511	Leu Arg Tyr Arg Asn Lys His Ile Cys Gly Ser Leu Ile Lys Glu	52
1632	UUG AGA UAC AGA AAU AAA CAU UGC CGG GGA GGA UCA UUG AUA AAG GAG	157
527	Ser Trp Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys	54
1680	AGU UGG GUU CUU ACU GCA CGA CAG UGU UUC CCU UCU CGA GAC UUG AAA	172
543	Asp Tyr Glu Ala Trp Leu Gly Ile His Asp Val His Gly Arg Gly Asp	55
1728	GAU UAU GAA GCU UGG CGU AAU CAU GAU GUC CAC CGG AGA GGA GAU	177
559	Glu Lys Cys Lys Glu Val Leu Asn Val Ser Glu Leu Val Tyr Gly Pro	57
1776	GAG AAA UGC AAA CAG GUU CUC AAU GUU UCC CAG CUG GUA UAU GGC CCU	162
575	Glu Gly Ser Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu	59
1824	GAA GGA UCA GAU CGU GUU UUA AUG AAG CGU CCU GCC AGG CCU GCJ GUC CUG	187

FIG. 12 (cont.)

591	Asp Asp Phe Val Ser Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile	60
1872	GAU GAU UUU GUU AGU ACC AUU GAU UUA CCU AAU UAU GGA UCC ACA AUU	191
607	Pro Glu Lys Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu	62
1920	CCU GAA AAC ACC AGU UGC AGU GUU UAU GGC UGG GGC UAC ACU GGA UUG	196
623	Ile Asn Tyr Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly	63
1968	AUC AAC UAU GAA GGC CUA UUA CGA GUG GCA CAU CUC UAU AUA AUG GGA	201
639	Asn Glu Lys Cys Ser Gln His His Arg Gly Lys Val Thr Leu Asn Glu	65
2016	AAU GAG AAA UCC AGC CAG CAU CCA CGG AAC GUG ACU CUG AAA GAG	206
655	Ser Glu Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu	67
2064	UCU GAA UUA UGU OCU GGG GCU GAA AAC AUU GGA UCA GGA CCA UGU GAG	211
671	Gly Asp Tyr Gly Pro Leu Val Cys Glu Gln His Lys Met Arg Met	68
2112	GGG GAA UAU GGU GGC CCA CUU GGU UGU GAG CAA CAU AAA AUG AGA AUG	215
687	Val Leu Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg	70
2150	GUU CUU GGU GUC AUU GUU CCU GGU CGU GGA UGU GCC AUU CCA AAA CGU	220
703	Pro Gly Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys	71
2208	CCG CGG AUU GGU CGA UAU UAU UAU GCA AAA UGG AUA CAC AAA	225
719	Ile Ile Leu Thr Tyr Lys Val Pro Gln Ser *** Leu Lys *** Val Cys	73
2256	AAU AUU UUA ACA UAU AAG GUA CCA CAG UCA UAG CUG AAG UAA GUG UGU	230
735	Leu Lys His Pro Pro Ile Gln Leu Ser Phe Thr *** Arg Phe Gln Arg	75
2304	CUG AAG CAC CCA CCA UAA CAA CUG UCU UUU ACA UGA AGA UUU CAG AGA	235
751	Met Trp Asn Leu Lys Cys His Leu Gln Gln Ser *** Asp Asn Tyr Trp	76
2352	AUG UGG AAU UUA AAA UGU CAC UUA CAA CAA UCC UAA GAC AAC UAC UGG	239
767	Arg Val Met Phe Val Glu Ile Leu Ile Asn Val Tyr Gly Cys Phe Leu	78
2400	AGA GUC AUG UUU GUU GAA AAU CUC AUU AAU GUU UAU GGG UGU UUU CUG	244
783	Leu Phe Cys Leu Ser Val Leu Phe Cys Gln Cys *** Ser Glu Leu Arg	79
2448	UUG UUU UGU UUG UCA GUG UUA UUU UGU CAA UGU UGA AGU GAA UUA AGG	248
799	Tyr Met Gln Val *** *** His Ile Ser *** Arg Tyr Leu Asn Gly Leu	81
2496	UAC AUG CAA GUC UAA UAA CAU AUC UCC UGA AGA UAC UUG AAA GGA UUA	254
815	Lys Lys His Thr Gly Ile Phe Ala Gly *** ***	82
2544	AAA AAA CAC ACA GCU UUA UUU GCU GGA UGA UGA UAA	257